

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2003, 19:52:03 ; Search time 44 Seconds

(without alignments)  
4074.113 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSEGPAGGGEVAELPG.....PRCDGHOQYPRKWRTPDAP 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4573	99.9	871	4 Q9HBC0	Q9hbc0 homo sapien
2	4571	99.9	871	4 Q9HBA0	Q9hba0 homo sapien
3	4570	99.8	871	4 Q96092	Q96q92 mus musculus
4	4393	96.0	871	11 Q9EPK8	Q9epk8 mus musculus
5	4387	95.8	871	11 Q9ES76	Q9es76 mus musculus
6	4378	95.7	871	11 Q9ER28	Q9er28 rattus norv
7	4374	95.6	871	11 Q9EQZ4	Q9eqz4 mus musculus
8	4334	94.7	873	11 Q9ERZ7	Q9erz7 mus musculus
9	4220	92.2	803	4 Q96RS7	Q96rs7 homo sapien
10	4087	89.3	803	11 Q91XR5	Q91xr5 mus musculus
11	3831	83.7	852	13 Q9DF53	Q9dfs3 gallus gall
12	1849	40.4	843	13 Q8QFN9	Q8qfn9 gallus gall
13	1819	39.7	838	11 Q9JMS7	Q9jms7 rattus norv
14	1818	39.7	838	11 Q35433	Q35433 rattus norv
15	1800	39.3	839	4 Q9NQ74	Q9nq74 homo sapien
16	1799	39.3	839	4 Q9NY22	Q9ny22 homo sapien

17	1795	39.2	839	4 Q9H304	Q9h304 homo sapien
18	1795	39.2	839	4 Q9H0G9	Q9h0g9 homo sapien
19	1693.5	37.0	528	11 Q92182	Q92182 rattus norv
20	1607.5	35.1	778	11 Q9JMS6	Q9jms6 rattus norv
21	1549	33.8	312	11 Q9CW94	Q9cw94 mus musculus
22	1497.5	32.7	761	11 Q9WUD2	Q9wud2 rattus norv
23	1495.5	32.7	761	11 Q9QYH8	Q9qyh8 rattus norv
24	1491	32.6	762	11 Q9JMI8	Q9jmi8 rattus norv
25	1469.5	32.1	756	11 Q9WTR1	Q9wtr1 mus musculus
26	1469.5	32.1	756	11 Q99K71	Q99k71 mus musculus
27	1467	32.1	764	4 Q9Y5S1	Q9y5s1 homo sapien
28	1459	31.9	721	11 Q9CVC7	Q9cvc7 mus musculus
29	1454.5	31.8	764	4 Q9Y670	Q9y670 homo sapien
30	1071	23.4	511	4 Q9H303	Q9h303 homo sapien
31	1041	22.7	468	11 Q920B4	Q920b4 rattus norv
32	1016	22.2	471	11 Q9JLM0	Q9jlm0 rattus norv
33	764.5	16.7	727	11 Q91WD2	Q91wd2 mus musculus
34	757.5	16.6	727	11 Q9R186	Q9r186 rattus norv
35	753.5	16.5	725	4 Q9H296	Q9h296 homo sapien
36	752.5	16.5	725	4 Q9H1D0	Q9h1d0 homo sapien
37	752.5	16.4	725	4 Q9H1D1	Q9h1d1 homo sapien
38	744.5	16.3	730	6 Q9XSM3	Q9xsm3 oryctolagus
39	742	16.2	729	4 Q9NOA5	Q9nqa5 homo sapien
40	735.5	16.1	723	11 Q9JUL2	Q9j12 rattus norv
41	730.5	16.0	723	11 Q9JIF0	Q9j10 rattus norv
42	598.5	13.1	557	4 Q8TDL3	Q8tdl3 homo sapien
43	584.5	12.8	729	11 Q9JJJ0	Q9jjj0 mus musculus
44	503.5	11.0	937	5 Q17469	Q17469 caenorhabdi
45	486.5	10.6	769	5 Q9N3Y9	Q9n3y9 caenorhabdi

#### ALIGNMENTS

RESULT 1

ID	Q9HBC0	PRELIMINARY;	PRT;	871 AA.
AC	Q9HBC0;			
DT	01-MAR-2001 (TREMREL. 16, Created)			
DT	01-MAR-2001 (TREMREL. 16, Last sequence update)			
DT	01-JUN-2002 (TREMREL. 21, Last annotation update)			
DE	OTRPC4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=KIDNEY CORTEX;			
RX	MEDLINE=20482174; PubMed=11025659;			
RA	Strotmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;			
RT	"OTRPC4, a nonselective cation channel that confers sensitivity to extracellular osmolarity."			
RL	Nat. Cell Biol. 2:695-702(2000).			
DR	EMBL; AF258465; AAG16127.1; -			
DR	InterPro; IPR002110; ANK.			
DR	InterPro; IPR000636; M-channel_trpL.			
DR	InterPro; IPR004729; Trp_Cachannel.			
DR	Pfam; PF00023; ank; 3.			
DR	Pfam; PF00520; ion_trans; 1.			
DR	SMART; SM00248; ANK; 3.			
DR	TIGRFAMS; TIGR00870; trp; 1.			
DR	PROSITE; PS50088; ANK_REPEAT; 1.			
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.			
DR	ANK repeat; Repeat.			
KW	SEQUENCE 871 AA; 98294 MW; C6205686DEAF6B6 CRC64;			

Query Match 99.9%; Score 4573; DB 4: Length 871;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 869; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTGGGAFFPLSSLANLFEFGDGLSPSPADASRPAGP 60

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Db 1 MADSSGPRAGPGEVAELPGDESGTGCGEAFPLSSLANLFEDEGSLSPADSRPAGP 60
Qy 61 GDGRPNLRMKFOGAFKRGVNPIDLLLESTLYESSVVPKPKAPMDSLFDTGTYRHSSDN 120
Db 61 GDGRPNLRMKFOGAFKRGVNPIDLLLESTLYESSVVPKPKAPMDSLFDTGTYRHSSDN 120
Qy 121 KWRKKIIEKQPSKPAPAPQPPILKVFNRPIFLDIVSRGSTADLDGLLFFLLTHKKRL 180
Db 121 KWRKKIIEKQPSKPAPAPQPPILKVFNRPIFLDIVSRGSTADLDGLLFFLLTHKKRL 180
Qy 181 TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Db 181 TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Qy 241 ALHAIERRCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Db 241 ALHAIERRCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Qy 301 VNYLTENPHKKADMRQDSRGNTVHLVAIAADNTRENTKFTVKMYDILLKLCARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVHLVAIAADNTRENTKFTVKMYDILLKLCARLPDS 360
Qy 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVSSLYD 420
Qy 421 LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLE 480
Db 421 LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLE 480
Qy 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDKLPKPCPV 540
Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDKLPKPCPV 540
Qy 541 NSLFDIGSFOLLFYIYSLVIVSAALYAGIAYLAVMVFALVGLMNNALYFTRGLKLTG 600
Db 541 NSLFDIGSFOLLFYIYSLVIVSAALYAGIAYLAVMVFALVGLMNNALYFTRGLKLTG 600
Qy 601 TYSIMIQIKILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIQIKILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Qy 661 RDSETFSTFLDLFKLTIGMDLEMLSSTKYPVVFILLVYIILFVLLNMLIALMGE 720
Db 661 RDSETFSTFLDLFKLTIGMDLEMLSSTKYPVVFILLVYIILFVLLNMLIALMGE 720
Qy 721 TVGVSKESKHIWKLQWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCFRV 780
Db 721 TVGVSKESKHIWKLQWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCFRV 780
Qy 781 DEYNWSHWNQNLGIINEDPGKNETYQYGFSTVGRLLRRDRWSVVRVVELNKNNSNPD 840
Db 781 DEYNWSHWNQNLGIINEDPGKNETYQYGFSTVGRLLRRDRWSVVRVVELNKNNSNPD 840
Qy 841 VVYPLDSMGNPRCDGHQOQYPRKWRDADAP 870
Db 841 VVYPLDSMGNPRCDGHQOQYPRKWRDADAP 870
```

RESULT 2

```
Q9HBAO PRELIMINARY; PRT; 871 AA.
AC Q9HBAO;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel.
GN VROAC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
```

```
RNA SEQUENCE FROM N.A.
RX MEDLINE=20531888; PubMed=11081638;
RA Lledike W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA Sali A., Hudspeeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT candidate voltage-gated osmoreceptor."
RL Cell 103:525-535 (2000).
DR EMBL: AF263323; AAC28029.1; -
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000636; Cat_channel_TripL.
DR InterPro: IPR004729; M+channel_nlg.
DR Pfam: PF00023; ank; 3.
DR Pfam: PF00520; ion_trans; 1.
DR SMART: SM00248; ANK; 3.
DR TIGRFAMs: TIGR00870; trip; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Receptor; Repeat.
SQ SEQUENCE 871 AA; 98265 MW; A86FB6ECC9103C19 CRC64;
```

Query Match 99.9%; Score 4571; DB 4; Length 871;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 868; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MADSSGPRAGPGEVAELPGDESGTGCGEAFPLSSLANLFEDEGSLSPADSRPAGP 60
Db 1 MADSSGPRAGPGEVAELPGDESGTGCGEAFPLSSLANLFEDEGSLSPADSRPAGP 60
Qy 61 GDGRPNLRMKFOGAFKRGVNPIDLLLESTLYESSVVPKPKAPMDSLFDTGTYRHSSDN 120
Db 61 GDGRPNLRMKFOGAFKRGVNPIDLLLESTLYESSVVPKPKAPMDSLFDTGTYRHSSDN 120
Qy 121 KWRKKIIEKQPSKPAPAPQPPILKVFNRPIFLDIVSRGSTADLDGLLFFLLTHKKRL 180
Db 121 KWRKKIIEKQPSKPAPAPQPPILKVFNRPIFLDIVSRGSTADLDGLLFFLLTHKKRL 180
Qy 181 TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Db 181 TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Qy 241 ALHAIERRCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Db 241 ALHAIERRCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Qy 301 VNYLTENPHKKADMRQDSRGNTVHLVAIAADNTRENTKFTVKMYDILLKLCARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVHLVAIAADNTRENTKFTVKMYDILLKLCARLPDS 360
Qy 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVSSLYD 420
Qy 421 LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLE 480
Db 421 LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLE 480
Qy 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDKLPKPCPV 540
Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDKLPKPCPV 540
Qy 541 NSLFDIGSFOLLFYIYSLVIVSAALYAGIAYLAVMVFALVGLMNNALYFTRGLKLTG 600
Db 541 NSLFDIGSFOLLFYIYSLVIVSAALYAGIAYLAVMVFALVGLMNNALYFTRGLKLTG 600
Qy 601 TYSIMIQIKILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIQIKILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Qy 661 RDSETFSTFLDLFKLTIGMDLEMLSSTKYPVVFILLVYIILFVLLNMLIALMGE 720
Db 661 RDSETFSTFLDLFKLTIGMDLEMLSSTKYPVVFILLVYIILFVLLNMLIALMGE 720
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QY 721 TVGVSKESKHIWKLQWATTILDIERSFPVFLRKAFRSGEMVTGKSSDGTDDRWCPRV 780
DB 721 TVGVSKESKHIWKLQWATTILDIERSFPVFLRKAFRSGEMVTGKSSDGTDDRWCPRV 780
QY 761 DEVNWSHWNQNGIINEDPGKNETYYGFSHTVGLRRDRSSVVRVVELKNSNPDE 840
DB 761 NEVNSHWNQNGIINEDPGKNETYYGFSHTVGLRRDRSSVVRVVELKNSNPDE 840
QY 841 VVPLDSMGNPRCDGQGGYPRKWRRTDDAP 870
DB 841 VVPLDSMGNPRCDGQGGYPRKWRRTDDAP 870

RESULT 3
Q96Q92
ID Q96Q92 PRELIMINARY; PRT; 871 AA.
AC Q96Q92: 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vanilloid receptor like channel-2.
GN VRL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishibashi K.;
RT "Molecular cloning of a new member of vanilloid receptor channel-like
RT proteins.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032427; BAB69040.1;
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat_channel_Trpl.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR004729; Trp_CaChannel.
DR Pfam: PF00023; ank; 3.
DR Pfam: PF00520; ion_trans; 1.
DR TIGRFAMs: TIGR00870; trp; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT; 1.
DR ANK repeat; Receptor; Repeat.
SQ SEQUENCE 871 AA; 98266 MW; C62056A401ECA8B6 CRC64;

Query Match 99.8%; Score 4570; DB 4; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 869; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADSSEGPRAGGVAELPGDESGTPGGEAPPLSLANLFEDEGSLSPADASRPAGP 60
DB 1 MADSSEGPRAGGVAELPGDESGTPGGEAPPLSLANLFEDEGSLSPADASRPAGP 60
QY 61 GGRPNLRMKFOGAFKGVGNPNDLLESTLYESSVVGPKKAPMDSLFYGYTRHSSDN 120
DB 61 GGRPNLRMKFOGAFKGVGNPNDLLESTLYESSVVGPKKAPMDSLFYGYTRHSSDN 120
QY 121 KWRKKIIEKQSPKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLPPELLTHKKRL 180
DB 121 KWRKKIIEKQSPKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLPPELLTHKKRL 180
QY 181 TDEEREPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFFINSPPFDIYYRGOT 240
DB 181 TDEEREPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFFINSPPFDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLYVAQADVHAQAGRFQPKDEGGYFYFGELPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLYVAQADVHAQAGRFQPKDEGGYFYFGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIDNTRENTKFTVMYDLLLLKCARLFPDS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIDNTRENTKFTVMYDLLLLKCARLFPDS 360

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## RESULT 4

```

Q9EPK8
ID Q9EPK8 PRELIMINARY; PRT; 871 AA.
AC Q9EPK8: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Transient receptor potential protein 12.
GN TRPV4 OR OTRPC4 OR TRP12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=20547522; PubMed=11094154;
RA Wissenbach U., Boedding M., Freichel M., Flockerzi V.;
RT "Trp12, a novel Trp related protein from kidney.";
RL FEBS Lett. 485:127-134(2000).
DR EMBL: AJ296078; CAC20703.1;
DR MGD; MGI:1926945; Trpv4.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat_channel_Trpl.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR004729; Trp_CaChannel.
DR Pfam: PF00023; ank; 3.
DR Pfam: PF00520; ion_trans; 1.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs: TIGR00870; trp; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT; 1.
DR ANK repeat; Receptor; Repeat.
SQ SEQUENCE 871 AA; 98026 MW; 5BAC6E33F99CEA05 CRC64;

```

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Query Match      96.0%; Score 4393; DB 11; Length 871;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 829; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSSLANLFEGEGDGLSPDASRRPAGP 60
Db 1 MADPGDGPRAAPGVAEPGDESGTSGGAFFPLSSLANLFEGEGDGLSPDASRRPAGP 60

Qy 61 GDGRPNLRMKFQGAFRKGVNPIDLLLESTLYESSVWPGPKAPMDSLFDTGYTRHHSSDN 120
Db 61 GDGRPNLRMKFQGAFRKGVNPIDLLLESTLYESSVWPGPKAPMDSLFDTGYTRHHSSDN 120

Qy 121 KWRKKTIKQPOSPKAPAPOPPPILAVENRPIIDLVSRGSTADLDGLLPLFLTHKKRL 180
Db 121 KWRKKVVEKQPOSPKAPAPOPPPILAVENRPIIDLVSRGSTADLDGLLPLFLTHKKRL 180

Qy 181 TDEEFREPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Db 181 TDEEFREPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240

Qy 241 ALHTAERRCKKHVVELLVAGQADVHAQARGRFQPKDEGGYFYFGEGLPLSLAACTNPHI 300
Db 241 SLHTAERRCKKHVVELLVAGQADVHAQARGRFQPKDEGGYFYFGEGLPLSLAACTNPHI 300

Qy 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKFTVMYDILLLKCARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKFTVMYDILLLKCARLPDS 360

Qy 361 NLEAVLNNDGLSPLMAAAKTGKIGIFQHIIRREVTDDETRHLSRKFKDWAYGPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMAAAKTGKIGVFOHIIRREVTDDETRHLSRKFKDWAYGPVSSLYD 420

Qy 421 LSSLDTCGCEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINWVSYLE 480
Db 421 LSSLDTCGCEVSVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINWVSYLE 480

Qy 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540

Qy 541 NSLFDGSGFOLLFYIYSLVIVSAALYAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Db 541 NSLFDGSGFOLLFYIYSLVIVSAALYAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600

Qy 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVTLNPNCTNMKYCDEDSNCTVPTYPAC 660
Db 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVTLNPNCTNMKYCDEDSNCTVPTYPAC 660

Qy 661 RDESETFTLDFLTKTIGMDLEMSSTKYPVVFIILLVYIILTFVLLNMLIALMGE 720
Db 661 RDESETSAFLDLTKTIGMDLEMSSTKYPVVFIILLVYIILTFVLLNMLIALMGE 720

Qy 721 TVGOVSKESHIKWLQWATTILDIERSFPVFLRKAFRSGEMVTYVGSDDGTPDRMCFV 780
Db 721 TVGOVSKESHIKWLQWATTILDIERSFPVFLRKAFRSGEMVTYVGSDDGTPDRMCFV 780

Qy 781 DEVNWSHWNQNLGIINEDPKNETYQYGFSTVGRRLRRRWSVPRVVELKNKSNPDE 840
Db 781 DEVNWSHWNQNLGIINEDPKNETYQYGFSTVGRRLRRRWSVPRVVELKNKSNPDE 840

Qy 841 VVYPLDGMGNPRCDGHOOGYPRKWRITDAP 870
Db 841 VVYPLDNLGNPCDGHOOGYAPKWRITDAP 870
```

RESULT 5

Q9ES76

ID Q9ES76 PRELIMINARY; PRT; 871 AA.

AC Q9ES76; 2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE OTRPC4 cation channel.

```
GN TRPV4 OR OTRPC4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEV;
RX MEDLINE=20482174; PubMed=11025659;
RA Strotenmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;
RT "OTRPC4, a nonselective cation channel that confers sensitivity to
RT extracellular osmolarity.";
RL Nat. Cell Biol. 2:695-702(2000).
DR EMBL: AF208026; AAG17543.1;
DR MGD; MGI:1926945; trpv4.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR004729; Trp_CaChannel.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMS; TIGR00870; trp; 1.
DR PROSITE; PS00088; ANK_REPEAT; 1.
DR PROSITE; PS02097; ANK_REPEAT; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 871 AA; 98069 MW; 2B28D554083F00A CRC64;

Query Match      95.8%; Score 4387; DB 11; Length 871;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 828; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSSLANLFEGEGDGLSPDASRRPAGP 60
Db 1 MADPGDGPRAAPGVAEPGDESGTSGGAFFPLSSLANLFEGEGDGLSPDASRRPAGP 60

Qy 61 GDGRPNLRMKFQGAFRKGVNPIDLLLESTLYESSVWPGPKAPMDSLFDTGYTRHHSSDN 120
Db 61 GDGRPNLRMKFQGAFRKGVNPIDLLLESTLYESSVWPGPKAPMDSLFDTGYTRHHSSDN 120

Qy 121 KWRKKTIKQPOSPKAPAPOPPPILAVENRPIIDLVSRGSTADLDGLLPLFLTHKKRL 180
Db 121 KWRKKVVEKQPOSPKAPAPOPPPILAVENRPIIDLVSRGSTADLDGLLPLFLTHKKRL 180

Qy 181 TDEEFREPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Db 181 TDEEFREPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240

Qy 241 ALHTAERRCKKHVVELLVAGQADVHAQARGRFQPKDEGGYFYFGEGLPLSLAACTNPHI 300
Db 241 SLHTAERRCKKHVVELLVAGQADVHAQARGRFQPKDEGGYFYFGEGLPLSLAACTNPHI 300

Qy 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKFTVMYDILLLKCARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKFTVMYDILLLKCARLPDS 360

Qy 361 NLEAVLNNDGLSPLMAAAKTGKIGIFQHIIRREVTDDETRHLSRKFKDWAYGPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMAAAKTGKIGVFOHIIRREVTDDETRHLSRKFKDWAYGPVSSLYD 420

Qy 421 LSSLDTCGCEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINWVSYLE 480
Db 421 LSSLDTCGCEVSVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINWVSYLE 480

Qy 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540

Qy 541 NSLFDGSGFOLLFYIYSLVIVSAALYAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Db 541 NSLFDGSGFOLLFYIYSLVIVSAALYAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600

Qy 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVTLNPNCTNMKYCDEDSNCTVPTYPSC 660
Db 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVTLNPNCTNMKYCDEDSNCTVPTYPSC 660
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Db 601 TYSIMTQKILFKDLFRLLVYLLFMIGYASALVTLNPNCTNMKVCEDQSNCTVPTYPAC 660
QY 661 ROSETSTFLLDLFKLTIGMDLEMLSSKYPVVFILLVTVIILTFVLLNMLALMGE 720
Db 661 ROSETSAFLDLDFKLTIGMDLEMLSSAKYPVVFILLVTVIILTFVLLNMLALMGE 720
QY 721 TVGOVSKESKHIWKLQWATTILDIERSPFVFLKAFRSGEMTVGKSSDGTDPDRRCFRV 780
Db 721 TVGOVSKESKHIWKLQWATTILDIERSPFVFLKAFRSGEMTVGKSSDGTDPDRRCFRV 780
QY 781 DEVNWSHWNQNLGIINEDPKNETYOYGFSGHTVGLRDRRWSVPRVVELNKNPNDE 840
Db 781 DEVNWSHWNQNLGIINEDPKSEIYQYGFSGHTVGLRDRRWSVPRVVELNKNSSADE 840
QY 841 VVPLDSMGPRCDGHQOQYPRKWRDDAP 870
Db 841 VVPLDNLGNPCDGHQOQYAPKWRDDAP 870

RESULT 6
Q9ER28 PRELIMINARY; PRT; 871 AA.
AC Q9ER28;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Vanilloid receptor-related osmotically activated channel.
GN VROAC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=20531898; PubMed=11081638;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT candidate vertebrate osmoreceptor.";
RL Cell 103:525-535(2000).
DR EMBL; AF263521; AAG28027.1; -.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat_channel_trpL.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR004729; Trp_CaChannel.
DR Pfam: PF00023; ank; 3.
DR Pfam: PF00520; ion_trans; 1.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMS; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat. Receptor. Repeat.
SQ SEQUENCE 871 AA; 98009 MW; 5D50684DA08C354B CRC64;

Query Match 95.7%; Score 4378; DB 11; Length 871;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 825; Conservative 22; Mismatches 23; Indels 0; Gaps 0;

QY 1 MADSSGPRAGPGEVAELPGDESGTPGGGAFLPSSLANLFEGEDGSLSPADASRPAGP 60
Db 1 MADPGDGPRAAGPDAEPGDESGTSGGGAFLPSSLANLFEGEGSSLSLPVDASRPAGP 60
QY 61 GDCRNLNRMKFOGATKGVNPNIDLLSTLYESSVVPKAPMDSLFDTGYTRHHUSON 120
Db 61 GDCRNLNRMKFOGATKGVNPNIDLLSTLYESSVVPKAPMDSLFDTGYTRHHUSON 120
QY 121 KWRKKIKTEKQSPKAPQPPPIKVFNRILLDIVSRGSTADLDGLLPHTHKKRL 180
Db 121 KWRKKIKTEKQSPKAPQPPPIKVFNRILLDIVSRGSTADLDGLLPHTHKKRL 180
QY 121 KWRKKIKTEKQSPKAPQPPPIKVFNRILLDIVSRGSTADLDGLLPHTHKKRL 180
Db 121 KWRKKIKTEKQSPKAPQPPPIKVFNRILLDIVSRGSTADLDGLLPHTHKKRL 180
QY 181 TDEEFPREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240

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Db 181 TDEEFPREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240
QY 241 ALHIAIERRCKKHVVELLVAGQADYHAQARGFPQPKDEGGYFFGELPLSLAACTNQPHI 300
Db 241 ALHIAIERRCKKHVVELLVAGQADYHAQARGFPQPKDEGGYFFGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADRRQDSRGNTVLHALVAIAIDNTRENTKFTVMYDLLLLKCARLFPDS 360
Db 301 VNYLTENPHKKADRRQDSRGNTVLHALVAIAIDNTRENTKFTVMYDLLLLKCARLFPDS 360
QY 361 NLSAVLNNDGLSLPMAAATGKTIGIFQHIIRREVTDDETRHLSRKFKDMAYGPVYSSLYD 420
Db 361 NLETVLNNDGLSLPMAAATGKTIGVFQHIIRREVTDDETRHLSRKFKDMAYGPVYSSLYD 420
QY 421 LSSLDTCGGEASVLEILVYNSKTENRHEMLAVPINELLRDKRKKGAVSFYINVSYL 480
Db 421 LSSLDTCGGEASVLEILVYNSKTENRHEMLAVPINELLRDKRKKGAVSFYINVSYL 480
QY 481 AMVIFTLAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFFTNFKDLFMKKCPGV 540
Db 481 AMVIFTLAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFFTNFKDLFMKKCPGV 540
QY 541 NSLFDGSQLLYFYIYSLVIVSAALYLAGIEAYLAVMFPALVGLWMNALYFTRGLKLTG 600
Db 541 NSLFDGSQLLYFYIYSLVIVSAALYLAGIEAYLAVMFPALVGLWMNALYFTRGLKLTG 600
QY 601 TYSIMTQKILFKDLFRLLVYLLFMIGYASALVTLNPNCTNMKVCEDQSNCTVPTYPAC 660
Db 601 TYSIMTQKILFKDLFRLLVYLLFMIGYASALVTLNPNCTNMKVCEDQSNCTVPTYPAC 660
QY 661 RDSETFSTFLLDLFKLTIGMDLEMLSSKYPVVFILLVTVIILTFVLLNMLALMGE 720
Db 661 ROSETSAFLDLFKLTIGMDLEMLSSAKYPVVFILLVTVIILTFVLLNMLALMGE 720
QY 721 TVGOVSKESKHIWKLQWATTILDIERSPFVFLKAFRSGEMTVGKSSDGTDPDRRCFRV 780
Db 721 TVGOVSKESKHIWKLQWATTILDIERSPFVFLKAFRSGEMTVGKSSDGTDPDRRCFRV 780
QY 781 DEVNWSHWNQNLGIINEDPKNETYOYGFSGHTVGLRDRRWSVPRVVELNKNPNDE 840
Db 781 DEVNWSHWNQNLGIINEDPKSEIYQYGFSGHTVGLRDRRWSVPRVVELNKNNGTDE 840

RESULT 7
Q9EQ24 PRELIMINARY; PRT; 871 AA.
AC Q9EQ24;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Ion channel.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Suzuki M.;
RT "Ion channel.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021875; BAA83731.2; -.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat_channel_trpL.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00023; ank; 3.
DR Pfam: PF00520; ion_trans; 1.

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Db 481 LCAMVFTLTAYTOPELEGPPYRTVDYLRAGEVITLFTGVLFEEFSIKDLFTKKCP 540
QY 539 GVNSLFDGSGFLLYFTYSVLIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRLGLKL 598
Db 541 GVNSLFDGSGFLLYFTYSVLIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRLGLKL 600
QY 599 TGYTSMIOKILFKDLFRLLVLLYLLFMIGYASALVSLNCPANMKVCNEDOTNCTVPTYP 658
Db 601 TGYTSMIOKILFKDLFRLLVLLYLLFMIGYASALVSLNCPANMKVCNEDOTNCTVPTYP 660
QY 659 SCRDSEFTFLDLFKLTIGMDLEMLSTKYPVVFIIILLVYIIILTFVLLNMLIALM 718
Db 661 ACKDSEFTSAFLDLFKLTIGMDLEMLSSAKYPVVFIIILLVYIIILTFVLLNMLIALM 720
QY 719 GETGVQSVKESKHWKQLQWATITLIDERSFPVFLKAFRSGEMVTVGKSSDGTDDRWC 778
Db 721 GETGVQSVKESKHWKQLQWATITLIDERSFPVFLKAFRSGEMVTVGKSSDGTDDRWC 780
QY 779 RVDEVNWSHWNQNLGIINEDPGKNEYQYGGFSGHTVGLRRDRWSSVPRVVELNKNNSP 838
Db 781 RVDEVNWSHWNQNLGIINEDPGKSEYQYGGFSGHTVGLRRDRWSSVPRVVELNKNNSA 840
QY 839 DEVVPLDSMGNPCDGHQGYPRKWRDAP 870
Db 841 DEVVPLDNLGNPCDGHQGYAPKWRDAP 872

RESULT 9
Q9RS7 PRELIMINARY; PRT; 803 AA.
ID Q96RS7
AC Q96RS7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2002 (TrEMBLrel. 19, Last sequence update)
DE Vanilloid receptor-like protein 2.
GN VRL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Derst C., Schafer M.K.;
RT "Cloning of mouse and human vanilloid receptor-like protein 2 (VRL-2).";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF279673; AAK69487.1; -.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR004729; Trp_CaChannel.
DR Pfam: PF00023; ank; 3.
DR Pfam: PF00520; ion_trans; 1.
DR TRIGRAMS; TIGR00870; trp; 1.
DR PROSITE; PS0088; ANK_REPEAT; 1.
DR PROSITE; PS0297; ANK_REPEAT; 1.
KW ANK repeat. Receptor. Repeat.
SQ SEQUENCE 803 AA; 91635 MW; AB329C595B325784 CRC64;

Query Match 92.2%; Score 4220; DB 4; Length 803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 802; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 MKFOGAFKGVNPNIDLESTLYESSVPGPKAPMDSLFDTGTRHHSSDNKRWRKKII 128
Db 1 MKFOGAFKGVNPNIDLESTLYESSVPGPKAPMDSLFDTGTRHHSSDNKRWRKKII 60
QY 129 EKQPSKAPAPQPPILKVFNRPIFLDIVSRGSTADLDGLLPFLLTTHKRLTDEEFREP 188
Db 61 EKQPSKAPAPQPPILKVFNRPIFLDIVSRGSTADLDGLLPFLLTTHKRLTDEEFREP 120
QY 189 STGKTCPLKALLNLNGRNDTIPVLLDIAERTGNMREFINSPRDIYRGOTALHIAIER 248
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Db 121 STGKTCPLKALLNLNGRNDTIPVLLDIAERTGNMREFINSPRDIYRGOTALHIAIER 180
QY 249 RCKHYVELLVAQADVHAQARGFPQKDEGGYFYFGEPLSLAACTNPHIYNYLTENP 308
Db 181 RCKHYVELLVAQADVHAQARGFPQKDEGGYFYFGEPLSLAACTNPHIYNYLTENP 240
QY 309 HKKADMRRODSRGNTVLHALVATADNTRNTRENTKFTKMYDILLKLCARLPDPSNLEAVLNN 368
Db 241 HKKADMRRODSRGNTVLHALVATADNTRNTRENTKFTKMYDILLKLCARLPDPSNLEAVLNN 300
QY 369 DGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPPYSSLYDLSLDTG 428
Db 301 DGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPPYSSLYDLSLDTG 360
QY 429 EASVLEILVYNSKIENRHEMLAVEPINELLRRKWKFGAVSFYINVSVLCAMVFTLT 488
Db 361 EASVLEILVYNSKIENRHEMLAVEPINELLRRKWKFGAVSFYINVSVLCAMVFTLT 420
QY 489 AYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIDLEMKKCPGVNSLFDGS 548
Db 421 AYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIDLEMKKCPGVNSLFDGS 480
QY 549 FOLLFYISVLIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRLGLKLGTYSIMIQ 608
Db 481 FOLLFYISVLIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRLGLKLGTYSIMIQ 540
QY 609 ILFKDLFRLLVLLFMIGYASALVSLNCPANMKVCNEDOTNCTVPTPSCRDSEFTST 668
Db 541 ILFKDLFRLLVLLFMIGYASALVSLNCPANMKVCNEDOTNCTVPTPSCRDSEFTST 600
QY 669 FLDDLFLKLTIGMDLEMLSTKYPVVFIIILLVYIIILTFVLLNMLIALMGETVGOVSKE 728
Db 601 FLDDLFLKLTIGMDLEMLSTKYPVVFIIILLVYIIILTFVLLNMLIALMGETVGOVSKE 660
QY 729 SKHWKQLQWATITLIDERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCFRVDEVNWSHW 788
Db 661 SKHWKQLQWATITLIDERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCFRVDEVNWSHW 720
QY 789 NONLGIINEDPGKNEYQYGGFSGHTVGLRRDRWSSVPRVVELNKNNSPDEVVPLDSM 848
Db 721 NONLGIINEDPGKNEYQYGGFSGHTVGLRRDRWSSVPRVVELNKNNSPDEVVPLDSM 780
QY 849 GNPDCDGHQGYPRKWRDAP 870
Db 781 GNPDCDGHQGYPRKWRDAP 802

RESULT 10
Q91XR5 PRELIMINARY; PRT; 803 AA.
ID Q91XR5
AC Q91XR5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vanilloid receptor-like protein 2.
GN TRPV4 OR VRL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY, BRAIN, AND HEART;
RA Derst C., Schafer M.K.;
RT "Cloning of mouse and human vanilloid receptor-like protein 2 (VRL-2).";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF279672; AAK69486.1; -.
DR MGD; MGI:1926945; Trpv4.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat_channel_nlg.
DR InterPro: IPR000636; M+channel_nlg.
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DR InterPro: IPR004729; Trp_CaChannel.
DR Pfam: PF00023; ank; 3.
DR TIGRFAMS: TIGR00870; trp; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR ANK repeat; Receptor; Repeat.
KW ANK repeat; Receptor; Repeat.
SQ SEQUENCE 803 AA; 91438 MW; 79A5BD9323300029 CRC64;

Query Match      89.3%; Score 4087; DB 11; Length 803;
Best Local Similarity 96.0%; Pred. No. 4.3e-309;
Matches 770; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

Qy 69 MKFGAPRKGVNPIDLLESTLYESSVVGPKKAPMDSLFDTYRHHSSDNKRKKII 128
Db 1 MKFGAPRKGVNPIDLLESTLYESSVVGPKKAPMDSLFDTYRHHSSDNKRKKVV 60

Qy 129 EKQPSKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLLPFLTHKKRLTDEEPREP 188
Db 61 EKQPSKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLLPFLTHKKRLTDEEPREP 120

Qy 189 STGKTCPLKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQTALHIAIER 248
Db 121 STGKTCPLKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQTSLSHIAIER 180

Qy 249 RCHHYVELLIAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQHIVNYLTENP 308
Db 181 RCHHYVELLIAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQHIVNYLTENP 240

Qy 309 HKKADMRQDSRGNTVHLVAIAADNTRENTKVTMYDLKLLKCARLPDLSNLEAVLNN 368
Db 241 HKKADMRQDSRGNTVHLVAIAADNTRENTKVTMYDLKLLKCARLPDLSNLEAVLNN 300

Qy 369 DGLSPLMMAAKTKIGIFQHIIRREVTDETRHLSRKFKDMWAGPVYSSLYDSSLDTCG 428
Db 301 DGLSPLMMAAKTKIGIFQHIIRREVTDETRHLSRKFKDMWAGPVYSSLYDSSLDTCG 360

Qy 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVVSYLCAMVFTLT 488
Db 361 EESVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVVSYLCAMVFTLT 420

Qy 489 AYTQLEGTPPYRTVDVLRAGEVITLFTGLVFFFTNIKDLFMKKCPGVNSLFDGS 548
Db 421 AYTQLEGTPPYRTVDVLRAGEVITLFTGLVFFFTSIKDLFTKKCPGVNSLFDGS 480

Qy 549 FQLLYFTYISLVIVSAALYLAGIEAVLAVMVFAVLGMNNAlyFTRGKLTGTYSIMIQ 608
Db 481 FQLLYFTYISLVIVSAALYLAGIEAVLAVMVFAVLGMNNAlyFTRGKLTGTYSIMIQ 540

Qy 609 ILFKDLFRLLVLLFWIGVASALVSLNINPCANKKVCNEDQTNCTVPTPSORDSETFT 668
Db 541 ILFKDLFRLLVLLFWIGVASALVSLNINPCANKKVCNEDQTNCTVPTPSORDSETFSA 600

Qy 669 FLDDLKLTIGMDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGETVGOVSKE 728
Db 601 FLDDLKLTIGMDLEMLSSAKYPVVFILLVYIILTFVLLNMLIALMGETVGOVSKE 660

Qy 729 SKHIWKQWATTILDIERSPPVFLKAFRSGEMVTYVCKSSDGTDPDRWCPRVDEVNWSH 788
Db 661 SKHIWKQWATTILDIERSPPVFLKAFRSGEMVTYVCKSSDGTDPDRWCPRVDEVNWSH 720

Qy 789 NONLGIINEDPGKNEYQYGFSTYVCLRRDRWSSVPRVVELNKNNSNPDEVVPLDSM 848
Db 721 NONLGIINEDPGKSEIYQYGFSTYVCLRRDRWSSVPRVVELNKNNSADEVVVPLDNL 780

Qy 849 GNPCCDCHQOQYPRKWRDTPDAP 870
Db 781 GNPCCDCHQOQYAPKWRDTPDAP 802

RESULT 11
Q9DFS3
ID Q9DFS3 PRELIMINARY; PRT; 852 AA.
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QY 496 GTPPYRTVDYLRAGEVITLFTGVLFETFTNFKDLFMKKCGVNSLFDIGSFQLLYFI 555  
Db 482 GPPPYRTTIDYLRAGEITLTLTGILFFESNIKOLFMMKKCGVNSFFDIGSFQLLYFI 541  
QY 556 YSVLVIVSAALYLAGEAVLAVMVFALVGLGWMNALYFTRGLKLTGTYSIMIQILFKDLF 615  
Db 542 YSVLVIVTAGLYGGVEAVLAVMVFALVGLGWMNALYFTRGLKLTGTYSIMIQILFKDLF 601  
QY 616 RFLVYLLFMIGYASALVSLNPNCAANNKVCNEDOTNCTVPTPSCRDSETFSTFLDLDFK 675  
Db 602 RELVYLLFMIGYASALVSLNPNCPSSCESDHSNCTLPTTPSCRDSETFSTFLDLDFK 661  
QY 676 LTIGMDLEMLSTKYPVVFIILLYIILTFVLLNMLIALMGFTVGQVSKESKHIWL 735  
Db 662 LTIGMDLEMLSAKYPGVFIILLYIILTFVLLNMLIALMGFTVGQVSKESKHIWL 721  
QY 736 QWATTILDIERSPFVFLKAFRSGEMVTYCKSDGTPDRRCFRVDEVNWSHWNQNLGII 795  
Db 722 QWATTILDIERSPFVFLKAFRSGEMVTYCKSDGTPDRRCFRVDEVNWSHWNQNLGII 781  
QY 796 NEDPGKNETYQYGFSGHTVGLRRDRWSVPRVVELNKNSPDEVVVPLDSNGNPRCDG 855  
Db 782 SEDPGKSDYQYGFSGHTVGLRRDRWSVPRVVELNKNSCPTEDVVVPLGTMGTAERE 841  
QY 856 HQGYPRKWRITDAP 870  
Db 842 RRHG-----QTPSSP 851

RESULT 12  
Q8QFN9 PRELIMINARY; PRT; 843 AA.  
AC Q8QFN9;  
DT 01-JUN-2002 (TremBLrel. 21, Created)  
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)  
DE Vanilloid receptor-like protein.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=DORSAL ROOT GANGLION;  
RX MEDLINE=21842900; PubMed=11853675;  
RA Jordt S.E., Julius D.;  
RT "Molecular basis for species-specific sensitivity to 'hot' chili  
peppers.";  
RL Cell 108:421-430(2002).  
DR EMBL; AY072909; AAL78069.1; -.  
KW Receptor.  
SQ SEQUENCE 843 AA; 96520 MW; ABB3592C9DC179C8 CRC64;

Query Match 40.4%; Score 1849; DB 13; Length 843;  
Best Local Similarity 47.3%; Pred. No. 6e-135;  
Matches 396; Conservative 144; Mismatches 215; Indels 82; Gaps 21;

QY 41 EGEDSLSPPADASRPAGGGRPNLRMKFGCAFRKGVNPNIDLLSTLY--ESSVPG 98  
Db 27 DGEDSAL--ETAD-----NLOGTF-----SNKVPKSKNIFARRGFEVNG 64  
QY 99 ---PKKAPMDSLFDY-----GTYRHSSDNKRKKIKTEKQp---QSPKAPAPQPPPTL 146  
Db 65 DCDKDNAPMDSFYQMDHLMAPSVIKFANMERGKLHLKLLSTDSITGCSKA-----F 116  
QY 147 KYVNPILFDIYSRGSTDADLGLPFLTHKKRLTDEEPREPSTGKTLKALLNLSNR 206  
Db 117 KYDRRRIFDVARGSTKDLDDLlyLNRLTKHLTDDEKPEKTEKTKLTKALLNHDGK 176  
QY 207 NDTIPVLLDIARTGNMREFTNSPFDIYYRQQTALHTAIERCKHYVELLIVAQADVHA 266  
Db 117 NDTIPVLLDIARTGNMREFTNSPFDIYYRQQTALHTAIERCKHYVELLIVAQADVHA 266

Db 177 NDTIPVLLDIARTGNMREFTNSPFDIYYRQQTALHTAIERCKHYVELLIVAQADVHA 236  
QY 267 QARGREFQP-KDEGGYFYFEGELPSLAACNTQPHIVNLTENPHKKAMRRDRSGNTVL 325  
Db 237 RACGEFFRIKKGPG-FYFEGELPSLAACNTQNLQIVKFLLENQYQAADTAEDSMGMWL 295  
QY 326 HALVATADNTRNTKFTVTKMYDILLKCARLPDPSNLEAVLNNDGSLPLMAAKTGKIGI 385  
Db 296 HTLVEIADNTKNTKFTVTKMYNIIILGAKINPILKEELTNKKGLTPLTAAKTGKIGI 355  
QY 386 FOHITREYTDTRHLSRKFEDWAGVPVSSLYDLSLDTGCEASVLEILVYNSKIEN 445  
Db 356 FAYILRREIKDECHLSRKFETWAGVPVHSSYDLSIDTC-EKNSVLEIIAYSETPN 414  
QY 446 RHEMLAVEPINELLRDKWRKFGAVSFYINVSVCAMVIFTTAYTQPLE--GTPPYPY- 502  
Db 415 RHEMLVPELNRLLQDKWDRFVKHLYFNFFVVAIHISILTTAAYRVPQKGDKPPFAFG 474  
QY 503 RTVDYLRAGEVITLFTGVLFETFTNFKDLFMKKCGVNSLFDIGSFQLLYFIYSLVIV 562  
Db 475 HSTGEYFRVTGETLSVLGLYFFFGIQ-YFVQRRPSLTKTLIVDSYSEVLFFVHSLLLS 533  
QY 563 SAALYLAGIEAVLAVMVFALVGLGWMNALYFTRGLKLTGTYSIMIQILFKDLFRFLVYL 622  
Db 534 SVLYFCGQELYVASMVFSALGWMNALYTRGFQOMGIYSVMIAKMLLRDLCLRFMEVYL 593  
QY 623 LEWIGYASALVSLNPNCAANNKVCNEDQ-TNCTVPTPSCRDSETFST-----FLDLDF 674  
Db 594 VFLLGFSTAVTILIED-----DNEQDNTSS--EYARSHTKRGFTSNLSYTCLELF 645  
QY 675 KLTIGMDLEMLSTKYPVVFIILLYIILTFVLLNMLIALMGFTVGQVSKESKHIWK 734  
Db 646 KFTIGMDLEFTENYRFSKSVFVILLVLYVILTYILLNMLIALMGFTVSKIAOESKIWK 705  
QY 735 LQWATTILDIERSPFVFLKAFRSGEMVTYCKSDGTPDRRCFRVDEVNWSHWNQNLGI 794  
Db 706 LQWATTILDIERSPFVFLKAFRSGEMVTYCKSDGTPDRRCFRVDEVNWSHWNQNLGI 765  
QY 795 INEDPG-----KNETYQYGFSGHTVGLRRDRWSVPRVVELNKNSP-----PDEV 841  
Db 766 INEDPGSGDLARNPSY-----CIKPGRVSGKNMKTLPVLLRDSRRRETPKLPPEI 817

RESULT 13  
Q9JM57 PRELIMINARY; PRT; 838 AA.  
AC Q9JM57;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)  
DE Vanilloid receptor type 1 like protein 1.  
GN VR1L1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tsuksumi S., Nakamura A., Kohama K.;  
RT "Vanilloid receptor type 1 like protein 1.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB040873; BAA94307.1; -.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR000636; Cat\_channel\_trpL.  
DR InterPro; IPR004729; Trp\_CaChannel.  
DR Pfam; PF00023; ank; 3.  
DR Pfam; PF00520; Ion\_trans; 1.  
DR SMART; SM00248; ANK; 3.  
DR TIGRFAMs; TIGR00870; trp; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW ANK repeat; Receptor; Repeat.



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Db 724 KLLQVFTDGGDYRCVDEVTNTWNTNNGIINEDPGNCEGVKRTLSFSLRSGRVS 783
QY 819 RDRWS--SVVP 827
Db 784 GRNKNFALVP 794

RESULT 15
Q9N074 PRELIMINARY; PRT; 839 AA.
AC Q9N074;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Vanilloid receptor 1.
GN VR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelsell R.E.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=20504379; PubMed=11050376;
RA Hayes P., Meadows H.J., Gunthorpe M., Harries M.H., Duckworth M.D.,
RA Cairns W., Harrison D.C., Clarke C., Ellington K., Prinjha R.K.,
RA Barton A.J., Medhurst A.D., Smith G.D., Topp S., Murdock P.,
RA Sanger G.J., Terrett J., Jenkins O., Benham C.D., Randall A.D.,
RA Gloger I.S., Davis J.B.;
RT "Cloning and functional expression of a human orthologue of rat
RT vanilloid receptor-1";
RL Pain 88:205-215(2000).
DR EMBL; AJ277028; CAB95729.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; Mchannel_nlg.
DR InterPro; IPR004729; Trp-CaChannel.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00520; ion_trans; 1.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMS; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Receptor; Repeat.
SQ SEQUENCE 839 AA; 94924 MW; 7142FEAE43189ECC CRC64;

Query Match 39.3%; Score 1800; DB 4; Length 839;
Best Local Similarity 44.9%; Pred. No. 3.9e-131;
Matches 374; Conservative.156; Mismatches 222; Indels 81; Gaps 15;

QY 49 PSPADASRPAGDGRPNL-----RMKFGQ-----AFKRGVNPIDLES--TLYESV 95
Db 22 PDPLDGDNSRPPPAKPOLSTAKSRTLFGKGDSEAFVDCPHEEGELDSCPTITVSPV 81
QY 96 V-----PGPKAPMDSLFYGYTHRHSSDNKNRKKTIIEKOPQSPKAPAPPPILKVF 149
Db 82 ITIQRPDGGTGARL-----LSQDSVAASTEKTRLY 113
QY 150 NRPILFDIVSRGSTDLDGLLPFLTHKKRLTDEFEPSGTGKTCPLKALLNSGRNDT 209
Db 114 DRRSIFEAVANNCDLESLLFLQKSKKHLTNEFKDPTGKTCCLKKAMLNLDHQNT 173
QY 210 IPIVLDIAERTGNREFNSPRDIYRGQTALHAIERRCKHYVELLVAOCADVHAQAR 269
Db 174 IPLLLEIARQDLSKELYNASYDYSYKGTALHAIERNWALVTLVENCADVQAAAH 233
QY 270-GRFPQKDEGGYFYFGEPLSLAACTNQPHIVNLTENPHKKADMRQDSRGNTVLHALV 329
Db 234 GDFKTKTKGRGFFYFGEPLSLAACTNQLGIVKFLQNSWQTADISARDSVGNVTVLHALV 293
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QY 330 AIADNTRENTKFTKMYDILLKLCARLFPDPSNLEAVLNNDGSLPLMAAKTKIGIFOHI 389
Db 294 EVADNTADTKFTVTSWYNELLILGAKLHPTLKEELTNKKGMTPLAALAGTAKIGVLAI 353
QY 390 IRREVTDETRHLSRRKFKDWAYGPVYSSLYSLSDTCGEASVLEILVY-NSKIENRHE 448
Db 354 LQREIQEPECRLSRKFTWAYGPVHSSLYDLSDICDTC-EKNSVLEVIAYSSSETPNRHD 412
QY 449 MLAVEPINELLRDKRKKFCVAFYINWVSYLCAWITFTTAYIQPLEGTPPYRTVDY 508
Db 413 MLVLEPLNRLQDKWDRFYFNFLVYCLYMIIFTMAAYRYPVDGLPPFKMEKMGDY 472
QY 509 LRLAGEVITLFTGVLFEEFTNIDLEMKKCPGVNSLFDIGSFOLLXYFIYSVLVTSAAVL 568
Db 473 FRVTGEILSVLGVYFFFRGIO-YFLQRRPSMKTLEVDYSSEMLFQLQSLFMLATVVLIF 531
QY 569 AGIEAYLAVMVFALVGLGMNALLYTRGLKLTGTYSIMIQILFKDLFRELLVLLFMIGY 628
Db 532 SHLKEYVASMVFSLAGWTNMLYTRGFQOMGIYAVNIEKMILRDLCLRFMFVYVFLPGF 591
QY 629 ASALVSLNPNCANMKVCNEDQTNCTVPTY-----PSCRSET-----FSTFLDLDFK 675
Db 592 STAVVTLI-----EDGKNDSLPESESTSHRWGPACRPDPDSYNSLYST-CLELEFK 640
QY 676 LTIGMGDLEMLSSTKYPVVFIIILVYIILTFVLLNMLIALMGETVGOVSKESKHIWKL 735
Db 641 FTIGMGDLEFTENYDFKAVFIILLAYVILTYILLNMLIALMGETVKNIAOESKNWKL 700
QY 736 QWATTILDIERSPVFLRKAFKRGEMVTYKSSDGTDRRMCFRVDEVNWSHWNQNLGII 795
Db 701 QRAITILDTEKSFLKCMRKAFKSGKLLQVYTPDGKDDYRMCFRVDEVNWTNTNTNVGII 760
QY 796 NEDPGKNE-TYQYGFSGHTVGLRRDRWS--SVVPRVVELN-----KNSNPDEV 841
Db 761 NEDPGNCEGVKRTLSFSLRSGRVMKNFALVPLLEASADRQSAQPEEV 813
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Search completed: June 3, 2003, 19:55:32  
Job time : 49 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2003, 19:52:38 ; Search time 26. Seconds

(without alignments)  
3216.806 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSSSEPRAGGEVAELPG.....PRCDGHQGGYPRKWRDAP 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1818	39.7	838	2 T09054	capsaicin receptor
2	1795	39.2	839	2 JC7621	capsaicin receptor
3	764.5	16.7	727	2 JC7796	epithelial calcium
4	757	16.5	723	2 JC7795	epithelial calcium
5	753.5	16.5	725	2 JC7531	calcium transport
6	503.5	11.0	937	2 T37241	olfactory channel
7	503.5	11.0	957	2 D8651	protein R0212.5 [1
8	445	9.7	900	2 T33026	hypothetical prote
9	342.5	7.5	790	2 T20312	hypothetical prote
10	278	6.1	519	2 T24772	hypothetical prote
11	235.5	5.1	1188	2 T19552	hypothetical prote
12	188	4.1	828	2 JC5807	trp3 protein - rat
13	148	3.2	1124	2 JH0588	calmodulin-binding
14	138.5	3.0	810	2 I38361	TRAC1 protein - hu
15	138	3.0	616	2 T00894	hypothetical prote
16	137	3.0	1765	2 T42388	sodium channel alp
17	136.5	3.0	683	2 A85044	hypothetical prote
18	136	3.0	2352	2 T30201	Notch homolog prot
19	134	2.9	481	2 T23729	hypothetical prote
20	134	2.9	1275	2 J00092	trp protein - fru
21	132	2.9	1274	2 JN0015	trp protein - fru
22	131.5	2.9	642	2 S58154	hypothetical prote
23	130.5	2.9	652	2 D85044	hypothetical prote
24	129.5	2.8	608	2 G02640	polycystic kidney
25	129	2.8	823	2 S44873	2C21.2 protein - C
26	127.5	2.8	643	2 D86167	protein F21B7.27 [
27	127.5	2.8	4377	2 A55575	ankyrin 3, long sp
28	126.5	2.8	2471	2 A49128	cell-fate determin
29	125.5	2.7	934	1 H71274	probable ankyrin -

30 125.5 2.7 2529 2 B64635 toxin-like outer m  
31 125 2.7 1957 2 S68453 sodium channel pro  
32 124 2.7 793 2 S68238 trp-1 protein - hu  
33 123.5 2.7 968 2 A37867 transcription fact  
34 123 2.7 751 2 F85043 hypothetical prote  
35 123 2.7 2212 2 A41098 calcium channel pr  
36 123 2.7 2531 2 T31070 notch homolog - se  
37 121 2.6 1549 2 T13940 ankyrin - fruit fl  
38 120.5 2.6 397 2 T46445 hypothetical prote  
39 120.5 2.6 573 2 D86464 F12G12.13 protein  
40 120.5 2.6 638 2 A56895 notch2 protein hom  
41 120 2.6 633 2 T27499 hypothetical prote  
42 119.5 2.6 574 2 T47566 hypothetical prote  
43 119.5 2.6 2108 2 S72458 sodium channel pro  
44 119 2.6 1765 2 T42714 ankyrin 3, splice  
45 119 2.6 1940 2 T42715 ankyrin 3, splice

RESULT 1  
T09054  
capsaicin receptor - rat  
N:Alternate names: vanilloid receptor subtype 1  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: T09054  
R:Caterina, M.J.; Schumacher, M.A.; Tomimaga, M.; Rosen, T.A.; Levine, J.D.; Juli  
Nature 389, 816-824, 1997  
A:Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway,  
A:Reference number: Z16539; MUID:98007969; PMID:9349813  
A:Accession: T09054  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-838 <CAT>  
A:Cross-references: EMBL:AF029310; NID:g2570932; PIDN:AAC53398.1; PID:g2570933  
A:Experimental source: dorsal root ganglion  
C:Keywords: ion channel; receptor

## ALIGNMENTS

Query Match	39.7%	Score	1818;	DB 2;	Length	838;
Best Local Similarity	45.6%	Pred. No.	1e-123;			
Matches	388;	Conservative	141;	Mismatches	222;	Indels 100; Gaps 18;
Qy	16	AELPGDESGTPGGE-----	-----	APFLSSLANLFEGEDGSLSPSPADA	54	
Db	5	ASLDSESESPPOENSECLDPPDRDCKPPVPHPTTRSRTRLF	-----	KGKDSSEASPLDC	63	
Qy	55	SRPAGPGDGRPNLRMKFQGAFRKGVNP	-----	PIDLLESTLYESSVVPKPKAPMDSLFDYGT	113	
Db	64	PYEEG-----	-----	GLASCPITVSSVL-----	TIQRGCDG-----	ASV 94
Qy	114	RHSSDNKRWRKIIIEKQOSKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPFL	173			
Db	95	RPSQDS-----	-----	VSAGEKPP-----	RLYDRRSIFDAVQAQNCQELLESLLPFL	136
Qy	174	LTHKKRLTDEEFREPSTGKCLPKALLNLNSGRNDITPVLLDIAETGNNRREINSPFRD	233			
Db	137	QRSKRLTSEFKDQGTGKTLKAMNLHNGQNDIALDLLVARKTDSUKQFVNASYTD	196			
Qy	234	IYRGOTALHAIATERCKHVVELLVAGQADHVAQAGRRFFQPKDEGGYFYFGEPLSLAA	293			
Db	197	SVYKGOTALHAIATERNMVLTVLLVENGADVQAAGDFPKTKGRPGFYFGEPLSLAA	256			
Qy	294	CTNQPHIVNYLTENPHKKADMRQDSRGNTVLHALVAIAIDNTRENTKFTVKMYDILLKLC	353			
Db	257	CTNOLAIVKFLQNSQPADISARDSVGNVTLHALVEADVNTVDNTKFTVSMYNEILIG	316			
Qy	354	ARLFPDSNLEAVLNQGLSPLMAAKTGKIGIQHIIIRREVTDTRHLSRKKFDWAYGP	413			
Db	317	AKLHPTLKLEETNRKGLTPLAASSGKIGVLAYILOREIHEPECRHLSRKFTEWAYGP	376			
Qy	414	VYSSLYDLSLSDTCGEASVLEILTV	-----	NSKIENRHEMLAVEPTINELLRDKWRKFCVAFSEY	472	

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Db 377 VHSLLYDSCIDTC-EKNSVLEVIATYSSETPNRDMMLVLEPLNRLQDKWDRFVKRIFY 435
Qy 473 INVSYLCMAFIITLTAIYQLEGTPPYPTTV-DYLRLAGEVITLFTGVLFFFFTNIKO 531
Db 436 ENFFVYCLYMIIFTAAAYRPEGLPPYKLNKTVDYFRVTEILSVSGVYFFERGQ- 494
Qy 532 LFMKKCPGVNSLFDIGSQQLLYFIYVSVIYSAALYLAGIYALVWVYFALVGLGMNLY 591
Db 495 YFLORPRLSKLFLVDYSSEILFFVQSFLMVLVSVVLYFSQRKEYVASVMVSLANGTNM 554
Qy 592 FTRGLKLTGTYSIMOKILFKDLFRFLVYLLEFMIGVASALVSLNPPCANMKVCNEDOTN 651
Db 555 YTRGFOQMGYIYAVMIERKMLRDLCLRFMFVYLVFLGFSTAVVTII-----EDGKN 604
Qy 652 CTVP---TYPSCROS-----ETFTFLDLFLKLTIGMGDMLMSSTKYVYFILL 699
Db 605 NSLPWESTPHKCRGSACKPGNSYNSLYST-CLELFKFTIGMGDLEFTENYDFKAVFIILL 663
Qy 700 VTYILTFLVLLNMLIALMGTVGOVSKESKHIKWLQWATWILDIERSFPVFLKAPRSG 759
Db 664 LAYVILTIVILLNMLIALMGTVNKAQESKNIWKLORAITILDTESKFLKCMRKAPRSG 723
Qy 760 EMVTVGKSSDCTPDRRCFRVDEVNWSHWNQNLGIINEDPGKNE-TYQYGFSTVTVGLR 818
Db 724 KLLQVGFTPDGKDDYRMCFRVDEVNWTNTWNTNNGIINEDPGNCGVKRTLFSLSRSGRV 783
Qy 819 RDRWS--SWVP 827
Db 784 GRNKNALVP 794

RESULT 2
JC7621
A:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7621
R:Corrington, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.
Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A:Title: The tissue distribution and functional characterization of human VR1.
A:Reference number: JC7621; MUD:21139751; PMID:11243859
A:Contents: Dorsal root ganglia
A:Accession: JC7621
A:Molecule type: mRNA
A:Residues: 1-839 <COR>
A:Cross-references: GB:AF196175
C:Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a
its integrative activation by several noxious stimuli, and plays an important role in In
C:Genetics:
A:Gene: vrl
A:Map position: 17p13
C:Keywords: transmembrane protein
F:201-233/Domain: ankyrin #status predicted <ANK1>
F:248-280/Domain: ankyrin #status predicted <ANK2>
F:333-385/Domain: ankyrin #status predicted <ANK3>
F:433-455/Domain: transmembrane #status predicted <TM1>
F:477-495/Domain: transmembrane #status predicted <TM2>
F:508-531/Domain: transmembrane #status predicted <TM3>
F:543-569/Domain: transmembrane #status predicted <TM4>
F:578-597/Domain: transmembrane #status predicted <TM5>
F:624-644/Domain: pore loop #status predicted
F:656-684/Domain: transmembrane #status predicted <TM6>

Query Match 39.2%; Score 1795; DB 2; Length 839;
Best Local Similarity 44.8%; Pred. No. 4.9e-122;
Matches 373; Conservative 156; Mismatches 223; Indels 81; Gaps 15;
Qy 49 PSPADSRAPGPGGRPNL-----RMKFGQ-----AFRKGVPNPIDLLS--TLYESSV 95
Db 22 PDPLDGPNSRPPPAKPOLSTAKSRTRLFGKGDSEAFPPVDCPHEGELDSCTITVSPV 81
Qy 96 V-----PGPKAPMDSLSFDYGYRHHSSDNKRKRKIIIEKQPQSPRAPAPPPILKVF 149

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Db 82 ITIQRPDGPCTCARL-----LSQDSVAASTKXTURLY 113
Qy 150 NRPIFLDVTSGSTADLDGLPFLTHKKRLTDEEFREPSTGKTKLKPALLNLNGRNDT 209
Db 114 DRSIFPAVAGNQCODLESLLFLQSKKHLTDNEFKDPETGKTKCLLKAMLNLHGQNTT 173
Qy 210 IPVLLDIAERTGNMREFINSFPRDIYRGOTALTIAIERRKHVYVELLVAGADVAQAAR 269
Db 174 IPLLEIARQTDLSKELVNASYTSYKGTQALTIAIERRNMAVLTLLVENGADVQAAAH 233
Qy 270 GRFPQKDEGQYFFGELPLSLAACTNQPHTVNVLTENPHKKADMRQDSRGNTVHALY 329
Db 234 GDFPKTKGRGFYFEGELPLSLAACTNQLGIVKFLQNSMQTADISARDSVGNVJHALY 293
Qy 330 AIAENTRENTKVFVKMYDLLLLKCARLPDPSNLEAVLNNDGLSPLMAAKTKGKIGFOHI 389
Db 294 EVAONTADNTKFTVSMNEILMLCAKHLPTLKEELTNKKGMTPLAAGTKGKLCVLAYI 353
Qy 390 IRREVTDEDTRHLSRKFKDMAYGPVYSLSYDLSDTCGEEASVLEILVY-NSKIERNHE 448
Db 354 LQREIQEPCRHLSRKFTENAYGPVHSSLYDLSDCIDTC-EKNSVLEVIATYSSETPNRHD 412
Qy 449 MLAVEPINELLRDNRKFGAVSFYINVVSYLCAMVIFLTATAYTOPLEGTPPYPTTVDY 508
Db 413 MLLVEPLNRLQDKWDRFVKRIFYENFLVYCLYMIIFTMAAYYRPVDGLPPFKMEKIGDY 472
Qy 509 LRLAGEVITLFTGVLFFFFTNIKDLFMKKKPCVNSLFDIGSQQLLYFIYVSVLSAALYL 568
Db 473 FRVTEILSVLGGVYFFERGQ-YFLORRPSMKTLFVDSYSEMLFFQLSLFMLATVYLYF 531
Qy 569 AGIEAYLAVWVYFALVGLGMNLYTRGLKLTGYTSIMQILFKDLFRFLVLLVLFPMIGY 628
Db 532 SHLKEYVASVMVSLALGWTNMLYTRGFQMGYIYAVMIERKMLRDLCLRFMFVYLVFLGF 591
Qy 629 ASALVSLNPPCANMKVCNEDOTNCTVPTY-----PSCRDSET-----FSITFLDLFLK 675
Db 592 STAVVTII-----EDGKNSLPSSTSHRWGPACRPDPDSSVNSLYST-CLELFK 640
Qy 676 LTIGMGDMLSSSTKYPVVFIILLVYIITFVLLNMLIALMGTVGOVSKESKHIKWL 735
Db 641 FTIGMGDLEFTENYDFKAVFIILLVYIITFVLLNMLIALMGTVNKAQESKNIWKL 700
Qy 736 QWATITLIDERSFPVFLKAPRSGEMVTVGKSSDCTPDRRCFRVDEVNWSHWNQNLGII 795
Db 701 QRAITITLIDTEKSLKCMRKAPRSGKLLQVGTYPDGKDDYRMCFRVDEVNWTNTWNTN 760
Qy 796 NEDPGKNE-TYQYGFSTVTVGLRDRWS--SVVPRVVELN---KNSNPDEV 841
Db 761 NEDPGNCGVKRTLFSLSRSGRVGRHWNKFNALVPLDLREASARDRQAQPEEV 813

RESULT 3
JC7796
epithelial calcium channel 2, ECac2 - mouse
N:Alternate names: calcium T1; Cat1
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-2002 #sequence_revision 17-May-2002 #text_change 02-Apr-2002
C:Accession: JC7796
R:Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A:Title: Gene structure and regulation of the murine epithelial calcium channels E
A:Reference number: JC7796
A:Accession: JC7796
A:Molecule type: DNA
A:Residues: 1-727 <WEB>
A:Cross-references: GB:AF336378
C:Comment: This calcium channel plays an important role in active transcellular ca
relevant for in vivo calcium homeostasis.
C:Genetics:
A:Gene: ECac2
A:Map position: 6
A:Introns: 43/2; 76/1; 117/1; 163/1; 196/1; 253/3; 302/3; 373/3; 402/3; 428/2; 483

```



C:Genetics:  
A:Gene: Cat1  
A:Map position: 7q33-34  
C:Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane protein

Query Match 16.5%; Score 753.5; DB 2; Length 725;  
Best Local Similarity 31.9%; Pred. No. 1.7e-46;  
Matches 217; Conservative 106; Mismatches 250; Indels 107; Gaps 24;

QY 171 PELLTHK-----KRLDEEPR---EPSTGKTCPLKALL--NLSNGRNDIPVLLDIA 217  
DB 48 PLLAAKNDVQALANKLLYEDCKVHHRGAMGATALHIAALYDNL-----EAAMLMEEA 102

QY 218 ERTGNMREFPNPFDDIYRGOTATLHIAIERCKHYVELLVAAGDVAHQARGFPOPKD 277  
DB 103 P-----ELVFPMTSYEGQTALHIAVYVNMNMLVRALLARRASVSARATGTAFR-RS 155

QY 278 EGGYFYGFLPLSLAACTNQHIVNYLTENPHKKADMRQDSRGNTVHLHALVAIADNTR 337  
DB 156 PCNLIVFGHPLSFAACVNSEIIVRLIEH---GADIRAQDSLGNTVHLHLI-----LQP 207

QY 338 NTKFTVKMYDLLLLKCARLPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIIRREVTD 397  
DB 208 NKTFAOMYNLLSYDRHGDHLQPLDLVPHOGLTPFKLAGVEGNTVMFQHLMOQ----- 262

QY 398 DTRHLRSRKFOWAGPVYSSLYDLSLDTGCEASVLEILVYNSKIENRHEMLAVEPINE 457  
DB 263 -----RKHTQMTYGLSTLYDLTEIDSSGDEQSLELIITTKREAR-QILDQTPVKE 315

QY 458 LLRDKWRKFGVSVFINVSYLCAMVIFTLTAYQPLE-----GTPP-----Y 500  
DB 316 LVSLAKWKRYGRPYFCMLGAIYLYIICFTMCCYIYRPLRPTNNRTPSRDNTLLOKLLQE 375

QY 501 PYRTVDYLRAGEVITLFTGVLFETFTKDLFMKKKCPGVNSLF-----IDGSFOLLXYIY 556  
DB 376 AYMTPKDDIRLVELGTIVGAIILLVEVPDIFRM---GVTRFFGQTILGGPFPHLIITY 432

QY 557 SVLVTSVAALVLAGIEAVLAVMVFALVGLWMNALVFTGLKLTGTYSIMIOKILPKDLFR 616  
DB 433 AFWLVTWMLKLSASGEVWPMFALVGLWGMVMTFAFGFOMGLPFTIMOKMIFGDLMR 492

QY 617 FLLVYLLPMIGYASALVSNLPCANMKVCNEDQNC--TVPTYPSRCDSETFSTFLDLDFK 675  
DB 493 FCWLMAVYILGFASAFYIFQ-----TEDPELGHFYDYPMA---LSTF--ELF- 537

QY 676 LTIGMDLEMLSSKTKYPVVFILLVYIILFTVLLNMLIALMGTVGQVSKESKHIWKL 735  
DB 538 LTIIDGPANY--NVDLPFMSITYAAFAIATLMLNLLIAMMGDTHRWVAHERDELWRA 595

QY 736 QWATTILDIERSFPVFLKAFRSGBMVTVGKSSDGTDDRWCFRVDEVNHNQNLGII 795  
DB 596 QIVATVYMLERKLPCLMP--RSG-----ICGREYGLGD--RWFLRVED----- 635

QY 796 NEDPGKNETYQYGFSTVVG 815  
DB 636 RQDLNRQRIQRYAQAFHTRG 655

## RESULT 6

T37241  
olfactory channel protein osm-9 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: T37241  
R:Colbert, H.A.; Smith, T.L.; Bargmann, C.I.  
J. Neurosci. 17, 8259-8269, 1997  
A:Title: OSM-9, A novel protein with structural similarity to channels, is required for  
A:Reference number: 221639; MUID:97477445; PMID:9334401  
A:Accession: T37241  
A:Status: preliminary;  
A:Residues: 1-937 <COL>  
A:Cross-references: EMBL:AF031408; NID:g2642589; PIDN:AAB87064.1; PID:g2642590

C:Genetics:  
A:Gene: Osm-9  
A:Map position: IV  
C:Keywords: transmembrane protein

Query Match 11.0%; Score 503.5; DB 2; Length 937;  
Best Local Similarity 25.5%; Pred. No. 3.5e-28;  
Matches 171; Conservative 109; Mismatches 260; Indels 131; Gaps 22;

QY 233 DIYR-----GOTALHIAIERCKHYVELLVAAGDVAHQARGFPOPK-----DEG 279  
DB 163 DIYLGDEQFGQSALHIAIVHDDYETVSLLSKADVNARACGNFFLPEDFKLTNKTIDYQ 222

QY 280 GYFYFGEPLSLAACTNQHIVNYLTYE---NPHKKADMRQDSRGNTVHLHALVAIADNTR 336  
DB 223 GYAYGEYPLAFAACFGNKDIYDLILQGANPN-----LQDSFGNTILHMCV----- 269

QY 337 ENTKEVTKMYDLLLLKCARLPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIIRREVTD 396  
DB 270 --INYSMSYAVRHWAK--PAD--PHVNHAGFTPLTKLGRKQIFEMLE----- 318

QY 397 EDTRHLRSRKFOWAGPVYSSLYDLSLDTGCEASV---LEILVYNSKIENRHEMLAV 452  
DB 319 -----INKVEFRFSDMTCSAYPLNTLDTIQDGSNTYDSALMTVINGSTPEHLDMLGS 372

QY 453 EPINELLRDKWRKFGVSVFINVSYLCAMVIFTLTAYQPLEGTPPYPTTV---DYL 509  
DB 373 EVIQRLLADKWKAFQAQRKLIBRLVLLIVQLITLSIVYIRPTE--LPRLYMEDPQWDDYI 430

QY 510 RLAGVITLFTGVLF-----FFTNKIDLFMKKCPGVNSLFTIDGSFOLLX 553  
DB 431 RTACELLTILNCIIFVGVQGEITRTOGMRYLRNLKTPAKAVFCIANLFL----- 482

QY 554 FYISLVTSVAALVLAGIEAVLAVMVFALVGLWMNALVFTGLKLTGTYSIMIOKILPKD 613  
DB 483 ---LLCIPFRLMKKHEIEE--ALFVPALPQSNIFLFPFARSAKLTGFPVOMIYSMIAGD 536

QY 614 LFRLLVYLLPMIGYASALVSL--LNPCANMKVCNEDQNC-----TVPTYPSRCDSETFSS 667  
DB 537 MIRFAITSAIFLVFSQVYFVGVKMDAKOKLEDPNPHACRISGTYITY-----NTFP 590

QY 668 TFLDLRKLTLTGMDLEMLSSKTKYPVVFILLVYIILFTVLLNMLIALMGTVGQVSK 727  
DB 591 EFTTILFRASGGDYDEEFCANCYQALTKTLFLVYMFVMPIMINILIAMMGNTYTTVIA 650

QY 728 ESKHIWLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCFRVDEVNHNQ 787  
DB 651 QAERAKRQYQAIVMWLERS-----VCKERLAASOLEYSIRLQOEGSSG 694

QY 788 WN--QNLGIINDEPKNETYQYGFSTVVGRLRRD---RWSSVYPRVVELNKNNSPDEVVV 843  
DB 695 MEVRGLMYIKQT-----KKTRARQKQAIYNWKTIGRKVIHTIDKVGTEQAVL 742

QY 844 PLDSMGNPRCD 854  
DB 743 LLH--GHRDL 751

## RESULT 7

D88651  
protein B0212.5 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: D88651  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1995  
A:Accession: D88651  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-957 <STO>  
A:Cross-references: GB:chr\_IV; PIDN:AAC02569.1; PID:G2854148; GSPDB:GN00022; CESP:B0212.5  
A:Note: contains similarity to ankyrin repeats  
C:Genetics:  
A:Gene: B0212.5  
A:Map position: 4

```
Query Match      11.0%; Score 503.5; DB 2; Length 957;
Best Local Similarity 25.5%; Pred. No. 3.6e-28;
Matches 171; Conservative 109; Mismatches 260; Indels 131; Gaps 22;

QY 233 DIYR-----GQTALHAIERCKHYVELLVAGADVHAQARGFFQPK-----DSG 279
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 166 DYLGDQFGQSALHLAIHDDYETVSLILNSKADVNARACGNFELPEDFKLTNKITDQ 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 280 GYFYGELPLSLAACTNPHIVNYLTE---NPHKADMRRODSRGNTVLHALVAIADNTR 336
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 226 GRAYGEYPLAFACGKNDIYDLLOFGANFN-----LQDSFGNTILHMCV----- 272
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 337 ENTKEVTKMYDLLLKLKARLPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVD 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 273 --INVSMSYAVRHWA--PAD--PHVNHAGFTPLTKLGRKQIFEMLE----- 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 397 EDRHLRKRKQWAGPYVSYSLDSSDTCGEASV-----LEILVYNSKIENRHEMLAV 452
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 322 -----IMKVEFRFSDMTCSAYPLNTLDIOPDGTNYDSALMTVINGSTPEHLDMIGS 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 453 EPINELLRDKWRKFGAVSEYINVSYLCAWVFTLTAYYOPLEGTPPYPTV---DYL 509
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 EYIORLLADKAKFAORKLIERLVLLIQLITLSIVYIRPTE--LPRLYMEDPOWDYI 433
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 510 RLAGEVITLFTGVLF-----FFTNIKDLFMKKCPGVNSLFTDGSFQLLY 553
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 434 RTACELLTLNLCIFFVGYQQLGEIRTOGMRGLRNLTAPAKAVFCIANLFL----- 485
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 554 FYISVLVISAALYLAGIAYLAVVFLVGLMGNALYFTRGKLTGTYSIMOKILFKD 613
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 486 -----LLCIPFLMKKHEIEE--ALFVFLPGLSWIFLLFFARSAKLTGPVQMIYMIAGD 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 614 LRFLLVLLFMIGYASALVSL--LNPANMKVCNEDOTNC-----TVPTPSCRSEFIS 567
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 540 MIRFAIISAIPLVFSQVYFVGKMDAKQKLEDNPHACRTSGTYITY-----NTFP 593
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 668 TFLDLFLKLTGMGDMLEMLSSPKYPVFIILVTYIILTFVLLNKLALMGETVGQVSK 727
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 594 EFTFLFRASGGYDYEEFSCANYQALTKTLFVLYFVYPMINMILLAMGNTYTVIA 653
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 728 ESKHIWLOWATTILDIERSPPVFLRKAFRSGEMVTYVGSKSDGTPDRRCWCFRDEVNWSH 787
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 654 QAEKAWROQYAOIVMVLERS-----VGKERLAASQLEYSIRLDQEGSSG 697
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 788 WN-QNLGIIINEDPGKNETYQYGFSTVGRLLRD---RWSSVVPVVELNKNNSNPDEVV 843
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 698 MEVRGLMWIKOT-----KKTRARQKQAIYNNKTIKGRKVIHTIDKVGTEQAVL 745
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 844 PLDSMGNPRCD 854
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 746 LLH--GHDRLD 754
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 8

T33026  
hypothetical protein T09A12.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T33026  
R:Hawkins, J.; Fulton, B.; Gillam, B.  
submitted to the EMBL Data Library, February 1998  
A:Description: The sequence of C. elegans cosmid T09A12.  
A:Reference number: 221265  
A:Accession: T33026  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-900 <HAW>

A:Cross-references: EMBL:AF047660; PIDN:AAC04431.1; GSPDB:GN00022; CESP:T09A12.3  
A:Experimental source: strain Bristol N2; clone T09A12  
C:Genetics:  
A:Gene: CESP:T09A12.3  
A:Map position: 4  
A:Introns: 43/2; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 78

```
Query Match      9.7%; Score 445; DB 2; Length 900;
Best Local Similarity 24.8%; Pred. No. 5.8e-24;
Matches 181; Conservative 104; Mismatches 250; Indels 194; Gaps 29;
```

```
QY 189 STGKTCPLKALLNSGRNDTIPVLIDIAERTGNRMREFINSFPRDIY-----YRGOTALH1 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 154 SNGETIIGCLLHASDIIHNAVLKILDYYPKLLN-----DIHISEDYGLSPHLQ 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 A-IERRCKHYVELLVAGADVHAQARGFFQPKDE-----GGYF 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 204 AIINTDCK--LVYKFLKLGADVNSRCYGAFACDDQKASRTDSLEHEYVELSLKNTYTNM 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 283 YFCELPISLAACNTNPHIVNYLTENPHKADMRRODSRGNTVLHALVAIADNTRKTV 342
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 YLGEYPLSFAACLNQOPESPRLLA---FKANPAQDNTGNSVLHMCV-----IHENAMF 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 343 TKMYDILLIKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVDTRHL 402
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 K-----LALECG-----ASLRV--NKQSLSPILTAAKLAKKEMFDEILEGDSV----- 358
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 403 SRKFKDWAYGPVSYSLDSSDTCGE-----EASVLEILVYNSKIENRHEMLAVEPIN 456
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 -----WAYGDASSTAYPLAKITDINETTGELNEASLSLVYVGOTVE--HLELDGLLD 410
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 457 ELLRDKWRKFG---AVSFYINVSYLCAWVFTL-----TAYYOPLEG- 496
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 411 TLLEAKWEAFARNMIVSFTAFYICVFTATLRLPIGFSTEMTEGWINRSEPPFGR 470
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 497 -----TPPYPTTVDYLRAGE---YIRLVFELFVVI 528
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 471 YGKNSTLQOVKPVINATSRGLVSESEPLSQCHLRNWDPIPFANS--YIRLVFELFVVI 528
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 517 TLFTGVLFPTFNKIDLFMKKCPGVNSLF--IDGSPOLLFYISVLVISAALYLAGIAYL 575
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 529 GICGVQVDFDRDIKRGKRWNVLTAFPAKTKLTFLVLAIMPTRLACDLSVLLV 588
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 576 --AVMVFLVGLMGNALYFTRGKLTGTYSIMOKILFKDLFRFLVLLFMIGYASALV 633
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 DNVLITVTMTFTTHLYCYRIVRFGPFLMVYTIITDIFRMLITGIFLUMGFSQSF 648
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 634 SLLNPC---AN-MKVCNEDOTNCT-----VPTPSC--RDSETF- 667
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 LIFLSCEREANVKKLITDQSEASESGSDNKNFLTRQISAYDTAIVKNAEVENVMQSP 708
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 668 ----TFLDLFLKLTGMGDMLEMLSSPKYPVFIILVTYIILTFVLLNKLALMG---E 720
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 709 AFVRTFILTIGFTVLYRNALCPANTVMWIKGVVFIILFELFVSIMQFNMLIAMTRTYE 768
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 TVGQVSKESKHILQWATTILDIERSF-----PVFLRKAFAFGSEGMVTVCK 766
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 769 TIFQOLE-----YKQRAQVILMLELSLSPKHERHOYLLKYSRPTGNTKNTKRS---LVSK 821
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 767 SSDGTDPDRR 775
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 822 KSATSRDSK 830
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 9

T20312  
hypothetical protein F28H7.10 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T20312; T21533  
R:Matthews, P.  
submitted to the EMBL Data Library, June 1996

A:Reference number: Z19255  
A:Accession: T20312  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-790 <WIL>  
A:Cross-references: EMBL:274030; PIDN:CAA98449.1; GSPDB:GN00023; CESP:F28H7.10  
A:Experimental source: clone D1054  
R:Birks, M.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19435  
A:Accession: T21533  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-790 <WIL>  
A:Cross-references: EMBL:272508; PIDN:CAA96644.1; GSPDB:GN00023; CESP:F28H7.10  
A:Experimental source: clone F28H7  
C:Genetics:  
A:Gene: CESP:F28H7.10  
A:Map position: 5  
A:Introns: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 67

Query Match 7.5%; Score 342.5; DB 2; Length 790;  
Best Local Similarity 22.3%; Pred. No. 1.3e-16;  
Matches 167; Conservative 99; Mismatches 221; Indels 263; Gaps 30;

QY 152 PILEFIVSRGSTADLGLLPFLTHKKRL-----TDEFRE-----PSTGK 192  
DB 109 PNILDEPDQO-AEMAGDL-----KKALLDGGGKSKYREMWWSVDERGSMGE 161  
QY 193 TCLPKALLNLSNGRNDTIPVLLDTAERTGN-MREFFNSPRDIYRGQTALHAIERCK 251  
DB 162 NLIAICLQGSALHN-----LIARLINFPLKINDICVSEYGLSLPLHAIYNQDA 214  
QY 252 HYVELLVAOGADYHAQARGFPQKDE-----GGYFFGELPLS 290  
DB 215 QFTSLLRLGADLNQRCYGAFFCADDQKASRTDSLEHEFVELAKNTNYTGSYFGEYPLS 274  
QY 291 LAACNQPHVINYLTENPHKKADMRRQDSRGNTVHALVAIAADNTRENTKFTVMYDNL 350  
DB 275 FAICMGQHDLFMLLA---KKALSAQDTNGNTALH-LCVIHD-----KM-DML- 318  
QY 351 LKCARLPDPSNLEA-----VLNNDGLSPLMMAKTKGIGIFQHIIRREVTDTRHLSRK 405  
DB 319 -----DAVLEAGNIRLANKQNTALTALRLAK-----KTESIQHLE-- 356  
QY 406 FKDWAYGPVYSSYLDLSDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRKWK 465  
DB 357 -----LMDGLIEQILDEKKA 372  
QY 466 FGAVSFYINVSVYLCAMVITLTAAYQPLEGTPPYRTVD----- 507  
DB 373 YGRALWRLSLGFIFFYCCFVCAYMLRPPSSATTEHLTRGRINDDGETESTNSTYLNQWHA 432  
QY 508 -----YLRLAGEVITLFT---GVLFETNIKDL-----FMKCKPG 539  
DB 433 IDTQCHLMYSANPWTHGWFRGCEIMTIIVLFQILLDFGIRRGFKWFLKAFPA 492  
QY 540 VNSLFDGSQLLYFIYSVLIVISAALYAGIAYLAV-----MVFALVLGMMNALYFTRG 595  
DB 493 --KLMPKAP--LFIISIPCLACSFH-----EFFLTIDNTMAIISILLVTHFLYLMRA 544  
QY 596 LKITGYSIMQIKLFKDFRLLVLFLEMIGVASALVSLNPCANMKKVCNEDQNTCTVP 655  
DB 545 IPEVGPFLVMVYTIATDLVRFAMYSIFLVGFSQSFYLFTSC----- 589  
QY 656 TYPSCRDSETF-----STF-----LLDLFKLITGMGDL---EMLSTKYPVVF 695  
DB 590 -----RDSAIAKIDPMGSEFNMINENPVDALLRTFIMTIGESVLYREMSACDNFMWK 644  
QY 696 IILLVTVIILTFVLL--NMLIALMG---ETVQGVSKESHKHWKQWATTILDIERSF-- 748  
DB 645 IGLKLVIFETFSVLOFNLLIANMTTETIFLTRKE----WKQWQAIVLMLEMLGLSP 700

QY 749 -----PVFLRKAFRSGEMTVVGK 766  
DB 701 ASRKMHLLRYTRPTGINKRVRSYVYVSKGE 730

RESULT 10  
T24772  
hypothetical protein T10B10.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T24772  
R:Sims, M.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19934  
A:Accession: T24772  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-519 <WIL>  
A:Cross-references: EMBL:272514; PIDN:CAA96679.1; GSPDB:GN00028; CESP:T10B10.7  
A:Experimental source: clone T10B10  
C:Genetics:  
A:Gene: CESP:T10B10.7  
A:Map position: X  
A:Introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3

Query Match 6.1%; Score 278; DB 2; Length 519;  
Best Local Similarity 29.5%; Pred. No. 3.5e-12;  
Matches 89; Conservative 36; Mismatches 115; Indels 62; Gaps 10;

QY 216 IARTCNMREFINSPF-RDIYR--GOTALHIAIERCKHYVELLVAOGADYHAQARGRF 272  
DB 161 VKMTYRFKIVNDIFLSEYIASVGLSPHQIAIVNEDLEMYFLCKGADVHORCYGSF 220  
QY 273 FQPKDE-----GGYFFGELPLSLAECTNQPHIVNYLTENPHKK 311  
DB 221 FCADDQKASRTDSLEHEWVDLVOSTKYTGMYGVEYPLSFACTNQVDCFRLLRA---MK 277  
QY 312 ADMRRQDSRGNTVHALVAIAADNTRENTKFTVMYDNLKLCARLPDPSNLEAVLNNDGL 371  
DB 278 ADPNMPTDNGNTVLH-----LTVIHDLPFMFLAVALGANLH-VRNNKL 321  
QY 372 SPLMMAKTKGIGIFQHIIRREVTDTRHLSRKDWAYGPVYSSYLDLSDTCGEE- 430  
DB 322 TPLAALRAAKKHIIYDILE---CDMDI-----SWRYGPVCKAYPLNDVDTINESD 370  
QY 431 -----ASVLEILVYNSKIENRHEMLAVEPINELLRKWKRFKGFASVFINVSVYLCAMVIF 485  
DB 371 GSNLPSNVIANVYVGKVD--HLEFFDGLIEEVLESKWETFGKKQLFMSLAGVIYFLAVF 428  
QY 486 TL 487  
DB 429 YL 430

RESULT 11  
T19552  
hypothetical protein C29E6.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T19552  
R:Dobson, R.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19141  
A:Accession: T19552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1188 <WIL>  
A:Cross-references: EMBL:272504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C29E6.2  
A:Experimental source: clone C29E6  
C:Genetics:  
A:Gene: CESP:C29E6.2  
A:Map position: 4  
A:Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

Query Match 5.1%; Score 235.5; DB 2; Length 1188;  
Best Local Similarity 20.1%; Pred. No. 1.4e-08;  
Matches 168; Conservative 113; Mismatches 280; Indels 273; Gaps 37;

QY 124 RKIIKQPOSPKAPQPPPIIKVFNRPILFDIVSGSTADLD-----GLLPFLLT 175  
DB 418 RKNKETERSALKSPTRNTLRIVSEVDRVTMVNVDRDQNTPMHIVASNGYLEMMOLLOK 477  
QY 176 HKKRLT---DEEFEPSTGKTCCLKALLNL-----SNG 205  
DB 478 HGASITQVNEDE-----TALHRAAIGVROLLEWDIRLLMKDGMGNSALHLAARS 529  
QY 206 RNDTIPVLLDIAERTGNMREFINSFRDIYRGQTAHIAIERCKHYVELLVAQADVH 265  
DB 530 HDATTKVLLD-----NGADREAKNS-----YQ-KTPOVAVDSKLETORCLVAKGAIE 578  
QY 266 AQ-----ARGRFQPKDEGGYFYFGEPLPLSLAACNQHIVN 302  
DB 579 SSSDTKTVLHTAAYGNESIVRYFIAEGVTIDRDEEGKTAFD-----IAC-----624  
QY 303 YLTENPHKADMR---ODSRGNTVLHALVAIAD-----NTRENTKF---VTWKYDLL 349  
DB 625 ---ENDHK---DVARAELETQWKNLMPICDVIPLDKHRNPVNMKRRTPFTLLTKPELA 679  
QY 350 -----LLKCARLPDSNLEAVLNNDGLSPLMMAKTGKIGIFQHIIR-REVTDDETRHL 402  
DB 680 SFVMDNCIEKSEETDSTOSVAYNFEFLDDTYMRCVSDGDTGEOLGCKSADED----735  
QY 403 SRKFKWAGVPVYSSLYDSSDTCGEEASVLILVYN-----SKIENRHEMLAVPEINE 457  
DB 736 ---FKLEKDAQSVASYD-----RVYKYHPLKLMADAIEKLH--LLNHPLSK 776  
QY 458 -LLRDWRKRFAGSVFINVSYLCAMVIFETLTAAYOPLEGTPPYRTTVDYLRAGEVI 516  
DB 777 ALKRYKWNRLGRMPYFALFMYL--VFIVSLTOYVRHTKA-----PYNWNEESYDSE--828  
QY 517 TLEGTGLVFFFTNKIDLFMKKCPGVNSLFD-----GSQLLY-----553  
DB 829 -----YFDEN-----ETCPOINTTKPDVWVKIIQITLAVCQILVECFQPKFAVL 875  
QY 554 -----FIYSLVIV---SAALYLAGIEAYLAWVFAVLV--GWMNALYFTTGLKL 598  
DB 876 VMWENWIDCFIYSTATIYDFSECSATSGVRNQMOWILAALCFFGWINLFLPMKMPR 935  
QY 599 TGYSTIMQIKFLKDLFRLLVLLPMIGVASALVSLNPNCAKMKVCNEDOTNCTVPTYP 658  
DB 936 FGIVFVNFVDIV-KTFRFPFVFLVFIASFSSFYVIL-----972  
QY 659 SCRDSFTSTFLDLFLKLTGM-----GD-----LEMLSTKYPVVFILLVTYI 703  
DB 973 --QNRPEFSTIFMSPLKTVMMIGEFETGIFGHDETHAEKMGFAHTAVACALFFFC 1030  
QY 704 ILTFVLLNMLIALMGETVGVSKSHIWKLQWATILDIERSFPVFLRK-----754  
DB 1031 IIMTILNLLGLAVDDIKGVOEKAEKRLAMQVLDVLQIEASLHFFIORTKRYATCRY 1090  
QY 755 -AFRSGEMTVGKSSDGTDRRCFRVDEVNWSHWNQNLGI-INEDPGKNETVQ 806  
DB 1091 ATPPYKHKTKTGAG-----W-----WSNRRRRGLSVSTDPDEIDEME 1129

RESULT 12  
JC5807  
trp3 protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 07-May-1999  
C:Accession: JC5807  
R:Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I.  
Biochem. Biophys. Res. Commun. 240, 167-172, 1997  
A:Title: Expression and Characterization of a trp1 homolog from rat.  
A:Reference number: JC5807; MUID:98042538; PMID:9367904  
A:Accession: JC5807

A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-828 <PRE>  
A:Experimental source: brain  
C:Comment: This protein participates in store-operated Ca2+ entry into cells.  
C:Superfamily: TRPC3 protein

Query Match 4.1%; Score 188; DB 2; Length 828;  
Best Local Similarity 20.6%; Pred. No. 2.4e-05;  
Matches 137; Conservative 100; Mismatches 240; Indels 188; Gaps 31;

QY 210 IPVLLDIAERTGNMREFINSFRDIYRGQTAHIAIERCKHYVELL-----VAQADV 264  
DB 52 IPVVRKMLEBSRTLN--VNC-----VDYMGONALQAVGNEHLEVTTELLKKENLARIGDA 105  
QY 265 -----HAQARGFFQF---KDEGGYFYFGE-----LPISLAA 293  
DB 106 LLLAISKGVRIVVEAILSHPALAQOGLSPLEURDDD--FYDEDDTFRSPDITPILAA 163  
QY 294 CTNQPHIVNVL-----TENPH-----KKADMRROD-----SRGNTVLHALVAIADNT 335  
DB 164 HCHKYEVVHLLLLKGRTERPHDYLCRCADCAEKQRLMTFSHSRINAYKASPGVLSLS 223  
QY 336 RENTKFTVMYDILLKLCARLPDSNLEAVLNNDGLSPLMMAKTGKIGIF-----386  
DB 224 SEDPVLTALELSNELAKLA-----NIEKEFKND--YRKLSMOCKDFVVGVDLDCRDSEEV 276  
QY 387 OHIRREVVDDETRH-----LSR-----KFKDWAYGPVYSSLYDSSDTCGEEASV-433  
DB 277 EALNGDLSVEERHGHKASLSRVKLAIEYKFKVAPNCOOQLLTWYGNLSGREIAIK 336  
QY 434 -LEILVYNSKIENRHEMLAV-----EPINELLRDWRKRFAGSVFINVSYLCAMVIF 485  
DB 337 CLVVLVVALAL-----PFLAIGYWIAPCSRGLKILRSFPMKFAASFI-----FLGLLVF 387  
QY 486 TLTAAYQPLEGTPPYRTTVDYLRAGEV-ITLFTGV-LFFFTNKIDLFMKKCPGVNSL 543  
DB 388 NASDRP---EGITTLNITVIDYPKQIFRVTQFTWTEMLIMVVLGMMWSEC---KEL 441  
QY 544 FIDGSPQLYFYISVLVIVS-----AALYLAGIEAYLA-----576  
DB 442 WLEGPREYIVQLMNVNLDLSIFIAFTARFLAQATKAQYVDSHVQESDLEVTLPPEV 501  
QY 577 -----VMVFALVGLGMMNALYFTRGLKLTGYSTIMQIKFLKDLF 615  
DB 502 QYFTYARDKWLPSDPOIIEGLYAIIVLSFSRIAIVLPANESFGPLQISLGRTV-KDIF 560  
QY 616 RELVYLLPMIGVASALVSLNPNCAKMKVCNEDOTNCTVPTYPSCRDSEFTFLDLFLK 675  
DB 561 KFWLFIWVFLAFMIGMFIYSYLGAKV---DPAFTTV-----EESFKTLFWSIFG 609  
QY 676 LTIGMDLEMLST-KYPVVF-----ILLVTYILTFVLLNMLIALMGETVGVSKES 729  
DB 610 LS-----EVTSVLYADHKFTENIGYVLYGIYNTVMVVLNMLIAMINSSYQIEEDS 663  
QY 730 KHIWK 734  
DB 664 DYEMK 668

RESULT 13  
JH0588  
calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 01-Mar-2002  
C:Accession: JH0588  
R:Phillips, A.M.; Bull, A.; Kelly, L.E.  
Neuron 8, 631-642, 1992  
A:Title: Identification of a Drosophila gene encoding a calmodulin-binding protein  
A:Reference number: JH0588; MUID:9222293; PMID:1314616  
A:Accession: JH0588  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA



A:Residues: 1-1124 <PHT>  
A:Cross-references: GB:M88185; NID:9469057; PID:gl58715  
A:Experimental source: head  
C:Genetics:  
A:Gene: trpl  
A:Cross-references: FlyBase:FBgn0005614  
C:Superfamily: TRPC3 protein  
C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein  
F:341-362/Domain: transmembrane #status predicted <TM1>  
F:374-396/Domain: transmembrane #status predicted <TM2>  
F:462-479/Domain: transmembrane #status predicted <TM3>  
F:512-533/Domain: transmembrane #status predicted <TM4>  
F:549-572/Domain: transmembrane #status predicted <TM5>  
F:643-668/Domain: transmembrane #status predicted <TM6>  
F:710-727/Region: calmodulin binding #status predicted  
F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 3.2%; Score 148; DB 2; Length 1124;  
Best Local Similarity 19.0%; Pred. No. 0.03;  
Matches 148; Conservative 103; Mismatches 255; Indels 274; Gaps 36;  
QY 189 STGKTCLPKALLNLSGRNDTPVLLD-----IAERTG---NMREFINSPFRDIYR--- 237  
DB 24 SVGGCCVPLGLPQ-----PILLEKKEFLAVERGDMPNRRILQKALRHQHINIC 74  
QY 238 ----GQTALHAIERRCKHYVELLVAQAD-----VHAQ 267  
DB 75 MDPLGRALTLAIDNENLEMYVELLVGMVETKDALHAINAEFVEAVELLEHEELIYKE 134  
QY 268 ARGFRFQPKDEGGYFYGEL-PLSLAACTNQPHVNYLTEN-----PH----- 309  
DB 135 GEPSYQKVDINTAMFADITPLMLAAHKNFEILRLIDRGAAVPHDRCGCECVR 194  
QY 310 --KKAMRRQDSRGN-----TVLHALVAIADTNTKTF-----VTKN-----YDL 348  
DB 195 LTAEDSLRHSLSRNIYRALCSPSLICLTSNDPSSTAFQLSWELNRLALTEQCEKSEYMD 254  
QY 349 LLLKCARLFPD-----SNLEAVLNNDGSLPLMMAAKTGKIGFQHIIRREVTDETR 400  
DB 255 LRROCKFAVDLLDQTRTSNLAITLNYD-----POMSSVEPG-----DRM 295  
QY 401 HLSRKFKDWAYGP---VYSSLYDL-----SSLD--TCGEASV---LEI 436  
DB 296 SLTRLVQNAISYKQKFAHNSIQQLLSIWTDGLPGFRKRSIVDKVICIAOVAVFLPLYC 355  
QY 437 LVYNSKTENRHEMLAVEP INELLDRKWRKFGAVSYINVSYLCAMVIFTLTAYYQPLEG 496  
DB 356 LIYCAPNCRGTGQLMRKPF-----MKFLIHASSYLFELTILIVS----- 395  
QY 497 TTPYPTRTVDYLRAG-----EVTILFTGVLPFFFTNIDLF 533  
DB 396 -----QRADDDFVRIFGTRMKKELABEQELRQGTQPSKLEIYVMYVIGFWVEVEQEIF 450  
QY 534 MKKCPGVNSL-----FIDGFSOLLFYTSVLVIVSAALYLAGTE-----AYLAVNVE 580  
DB 451 ---AVGKSYLRNWNWIFDLRNSLY--VSVACLRAFAYIQOATEIARDPQMAVIPREK 505  
QY 581 -----ALVLGWMNALYFTRGLKLTGYSI-----MIQKILFK---DLFRLLYLLFMI 626  
DB 506 HFDPPQLIAEGLFAAANVFSALKVLHLSINPLGLQISLGRMVIDIVKFFIYTLVLF 565  
QY 627 GYASALVSLNPNCAKMKVCHNDQNTCTVPTYP-----SCRSEFSTFLLDLFK 675  
DB 566 AFACGLNOLLWYFAAL-----EKSICYV--LPGEADMGSHGSDCKMRFRG-----NLFE 614  
QY 676 LT-----IGMGOLEMSSLSTKYPWVF--IILLVTVYIILTVLNLMLIALMGVVGQ 724  
DB 615 SSQSLFWASFGWGLDDFELSGIKSYTRFWGLLMFGSYVINVLNLLIAMNSYAM 674  
QY 725 VKESKHIWKIQ-----WATTILDIERSFPVFLRKAFRSGEMVTYVSKSDGTPDRRCFRV 780  
DB 675 IDEHSDTEWKFAFTKLWMSYFEDSATLPPPF-----NVLPSYKWKVIRI 717

## RESULT 14

I38361  
TrpC1 protein - human  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 04-Sep-1998  
C:Accession: I38361  
R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.  
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995  
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.  
A:Reference number: I38361; MUID:96003837; PMID:7568191  
A:Accession: I38361  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-810 <RES>  
A:Cross-references: EMBL:X89066; NID:gl019786; PID:gl019787  
C:Superfamily: TRPC3 protein  
Query Match 3.0%; Score 138.5; DB 2; Length 810;  
Best Local Similarity 18.1%; Pred. No. 0.091;  
Matches 147; Conservative 126; Mismatches 315; Indels 223; Gaps 36;  
QY 12 PGEVAELPGDSEGTGPGGEAPFLSSLANLFECEGSLSPSPADASRPAGPGDGRPNLRMKF 71  
DB 3 PG-----IPGPRAEAAVGTTHFFSPGAWLGSQSGS---GPVGAPPPS----- 42  
QY 72 QGAFRKGVNPIDILLESTLYESSYVPGPKAPMDSLFDYGYTRHHSSDNKWRKKIIEKQ 131  
DB 43 -----PGLPPSWAAMMAALYPSTDLSGASSSL----- 70  
QY 132 POSKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLLPLLTTHKK---RLTDEEPRP 188  
DB 71 PSSPSSSSNEVMALK-----DVREKVEENTLNEKL-FLLACDKGDYMYMKKILEEN 121  
QY 189 STGK---TCLP-----KALLNLSGRNDTPVLLD-----IAERTGMREFINSPFRDIY 235  
DB 122 SSGDLNINCDVGLRNNAVTTIENENLDIQLLDYCCQKLMEIQNE---YSTTMDV- 177  
QY 236 YRGOTALHAIERRCKHYVELLVAQADV---HA-QARGRFQPKDEGGYFYGELPLSL 291  
DB 178 ----APVILAAHRNNEYILTMLLKQDVSLPKPHAVGCECTLCSAKNKKDSLRSRFRLDI 233  
QY 292 AACTNQPHVNYLTENPHKKADMRQDSRGNTVYLHALVAIAD-----NTRENT 339  
DB 234 YRCLASPALIMLTEDP-----ILRAFELSADLKELSLVEVEFRNDYEEL 278  
QY 340 KFTVMYDILLLLCARLFPDSNLEAVLNND-----GLSPLMMAAKTGKI 383  
DB 279 AROCKMFAKDLAQAAR--NSRELEVINLHNTSSDEPLDKRGLLEBMMNLSRLKAIKYN-- 334  
QY 384 GIFQHIIRREVTDETRHLRKRKFDWAYGPVYSLSYDLSLSDTCGEASVLEILVYNSKI 443  
DB 335 -----QKEFVSQSN---CQQLNTVM---FGMSGYRRKPTCKKIMTVLTGIF--- 377  
QY 444 ENRHEMLAVEPINELLRDKWRKFCGV-----SFYINVSYLCAMVIFTL-TAYYQPLEG 496  
DB 378 -----WPVLSLCYLIAPK-SQGRILHTPFMKFIHGASYFTFLLNLLNLSLYNEDKK 430  
QY 497 TTPYPTRTVDYLRAGLEVITLFTGVLPFFFTNIDLFMKKCPGVNSLFDIGSFOLLFYIY 556  
DB 431 NTMGPALERIDYL-----LILWIIGMI--NSDIKRLAYE---GLED-FLEESRNLQSFVM 479  
QY 557 SVLVIVSAALYLAG-----IEAYLVNV-----FALVLGWMNALYFTRGLK 598  
DB 480 NSLYLATFALKVVAHNKFDHFAKQDMDAFHTLVAEGLFAFANVLSYLRFFMYTTSSI 539  
QY 599 TGYISIMQIKLFDLFRLLVLLFMIGYASALVSLNPNCAKMKVCHNDQNTCTVPTYP 658  
DB 540 LGPLQISMGQML-ODFGKFLGMFLVLFSTIGLTQLYDKGYTSK-----EQKDC-VGIFC 593  
QY 659 SCRDESEFTSFLDLFLKLTIGMGDLEMLSTKYPVVFII-----ILLVTVI 703  
DB 594 EQSDNDFHSFICTCFAL-----FWIFSLAHVAIFVTRFSYGEELQSFVGAIVGTYN 647

Qy 704 ILTFVLLNMLIALMGETVGQVSKESKHMK 734  
Db 648 VVVVIVLTKLVLAMLHKSFOLIANHEDKWK 678

## RESULT 15

T00894  
hypothetical protein F21B7.8 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 22-Oct-1999  
C:Accession: T00894  
R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Cor  
eologis, A.; Ecker, J.R.  
Submitted to the EMBL Data Library, January 1998  
A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.  
A:Reference number: Z14208  
A:Accession: T00894  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-616 <SH1>  
A:Cross-references: EMBL:AC002560; NID:g2618677; PID:g2809239; GSPDB:GN00059; ATSP:F21B7  
C:Genetics:  
A:Gene: ATSP:F21B7.8  
A:Map position: 1  
A:Introns: 229/1; 411/3

Query Match 3.0%; Score 138; DB 2; Length 616;  
Best Local Similarity 19.2%; Pred. No. 0.066;  
Matches 136; Conservative 103; Mismatches 229; Indels 242; Gaps 32;  
Qy 161 GSPADLDGLPFLTHKRLTDEEFREPSTGKCLPKA--LLNLSNGRNDTIPVLLDIAE 218  
Db 17 GSLSDPDQWTF-----KKDESEIMNPAL--LCVARGDKVSLKRIKINDDVKTORLYD 69  
Qy 219 RTGN-----MREFINSPF-----RDIYRGQALHAIERRCKHYVELLV--- 258  
Db 70 NQNSILHIAAALGHVHIVEFIITFPNLLQNVNLMGETTLHVAARAGSLNIVEILVRFI 129  
Qy 259 -----AQAGD--VHAQAGR-----FFQPKDEGGYFY---- 283  
Db 130 TESSYDATIAKSKNGDTHAALKGKHVEAFCLVSVKHDVDFDKNNDEASPLYMAVE 189  
Qy 284 --FGELPLSLAQTNPQHVNYLVE-----NPHKKADMR-----RQD-----SRG 321  
Db 190 AGYHELVLKMLESSSPSILASMFSGKSVTHAAMKANRRDILGIVLRQDPGLIELNEEC 249  
Qy 322 NTVLHALVAIADNTRENTKVTWKYDLLLLKCARLPDSNLEAVLNNDGLSPLMMAAKTG 381  
Db 250 RTCLS--YGASMGCEGIRYLAEDF---KAA-----SSLCYVADDGFTPIHMAAKEG 298  
Qy 382 KIGIFOHIIR-----REVTDTRH-----LSRKFKNWAY-----GPVYSLYDLSS- 423  
Db 299 HVRIIRKFKHCPSRELLNNOCONIFHVAAGKSVKYLKLDGKRMNEQDINGN 358  
Qy 424 ----LDTGGEASVLEILVYNSKIENR---HEMLAVEPINELLRKDKRFGAVSFYINVY 476  
Db 359 TPLHLATKHRYPIVNVNKLWNGINLRALNNEGFTALDAETMKN-----NAVY-LY 410  
Qy 477 SYLCAMVIFTLTAYQP-----LEGTPPYPTVTDYDLRLAGEV---ITLFTGVLF 524  
Db 411 KRLIHWALVSAGAPHPNLIPLTVSQSSQSPERYKDSVNTLMVTATLVATVTFAGL-- 468  
Qy 525 FFTNIDKLPKKCP--GVNSLFDIGSFQLLYFIYVIVVSAALYLAGIAYLAVVWFAL 582  
Db 469 ---TLPGGYMSSAPHLGMAALVKNLKFVFLNNIACMTSVVTVNMAIWAQLG----- 519  
Qy 583 VLGMNVALYTRGLKLTGTYSIMQIKLFKDLFRFLVLLFMIGVASALVSLNFCANN 642  
Db 520 -----DALLTKAFRLALPLL-----TAVVSMN----- 543  
Qy 643 KVCNEDQTNCTVPTPSCRDSETFSTFLDLFKLTICMGDLEMLSTKYPVVFIIILVTY 702

Db 544 -----MASVAGLTIVVSDLPWLS-----HLVLDAIDS 569

Qy 703 ILTFVLLNMLIALMGETVGQVSKESKHMKLQWATTILDIERSPVFL 752  
Db 570 AFLVFLMLLIPIYAFSSTRHGFL-----RHIF-----YFPYFL 602

Search completed: June 3, 2003, 19:56:04  
Job time : 30 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2003, 19:51:13 ; Search time 14 Seconds

(without alignments)

2577.458 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSSGPRAGGEVAELPG.....PRCDGHOQGYPRKWRDAP 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	4.0	1172	1 TRP2_MOUSE	Q9r244 mus musculus
2	181.5	4.0	862	1 TRP7_HUMAN	Q9hcx4 homo sapien
3	178.5	3.9	862	1 TRP7_MOUSE	Q9hcx5 mus musculus
4	172	3.8	885	1 TRP2_RAT	Q9r283 rattus norv
5	166	3.6	981	1 TRP4_BOVIN	P79100 bos taurus
6	164	3.6	974	1 TRP4_MOUSE	Q9quq5 mus musculus
7	164	3.6	977	1 TRP4_HUMAN	Q9ubn4 homo sapien
8	161	3.5	977	1 TRP4_RAT	Q35119 rattus norv
9	155	3.4	1503	1 TRL2_HUMAN	Q94759 homo sapien
10	153	3.3	836	1 TRP3_MOUSE	Q9qzcl mus musculus
11	152.5	3.3	974	1 TRP5_RABIT	O62852 oryctolagus
12	150.5	3.3	973	1 TRP5_HUMAN	Q9ulb2 homo sapien
13	150.5	3.3	975	1 TRP5_MOUSE	Q9qx29 mus musculus
14	149.5	3.3	930	1 TRP6_MOUSE	Q61143 mus musculus
15	148	3.2	848	1 TRP3_HUMAN	O13507 homo sapien
16	148	3.2	1124	1 TRPL_DROME	P48994 drosophila
17	145	3.2	736	1 TRP2_RAT	Q9jmi9 rattus norv
18	143	3.1	931	1 TRP6_HUMAN	Q9y210 homo sapien
19	137	3.0	436	1 V245_FOWPY	Q9j425 fowipox vir
20	136.5	3.0	966	1 PKD2_MOUSE	O35245 mus musculus
21	135	2.9	1275	1 TRP_DROME	P19334 drosophila
22	134.5	2.9	968	1 PKD2_HUMAN	O13563 homo sapien
23	131.5	2.9	642	1 YAZA_SCHPO	Q09701 schizosacch
24	131.5	2.9	759	1 TRP1_RAT	Q9qx01 rattus norv
25	130.5	2.9	3056	1 ATM_HUMAN	O13315 homo sapien
26	129	2.8	823	1 YN52_CAEEL	P34586 caenorhabdi
27	128.5	2.8	759	1 TRP1_RABIT	Q9tun9 oryctolagus
28	127.5	2.8	4377	1 ANK3_HUMAN	O12955 homo sapien
29	126.5	2.8	768	1 YB23_HUMAN	Q9ulj7 homo sapien
30	126.5	2.8	2471	1 NTC2_RAT	Q9qk30 rattus norv
31	125.5	2.7	809	1 TRP1_MOUSE	P41056 mus musculus
32	124	2.7	793	1 TRP1_HUMAN	P48995 homo sapien
33	123.5	2.7	793	1 TRP1_BOVIN	O18784 bos taurus

#### ALIGNMENTS

##### RESULT 1

ID	TRP2_MOUSE	STANDARD:	PRT;	1172 AA.
AC	Q9R244; Q9R243; Q9ES60; Q9ES59;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Short transient receptor potential channel 2 (TrpC2) (mTrp2).			
GN	TRPC2 OR TRRP2 OR TRP2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Testis;			
RX	MEDLINE=99162557; PubMed=10051594;			
RA	Vannier B., Peyton M., Boulay G., Brown D., Qin N., Jiang M., Zhu X.,			
RA	Birnbaumer I.;			
RT	"Mouse trp2, the homologue of the human trpc2 pseudogene, encodes			
RT	mTrp2, a store depletion-activated capacitative Ca2+ entry channel.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:2060-2064(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).			
RX	PubMed=10998353;			
RA	Hofmann T., Schaefer M., Schultz G., Gudermann T.;			
RT	"Cloning, expression and subcellular localization of two novel splice			
RT	variants of mouse transient receptor potential channel 2.";			
RL	Biochem. J. 351:115-122(2000).			
CC	-1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE			
CC	CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A			
CC	PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR			
CC	TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. MAY ALSO BE			
CC	ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).			
CC	-1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1/A (SHOWN HERE), 2/B, 3/ALPHA			
CC	AND 4/BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: ISOFORM 3 IS UBQUITOUSLY EXPRESSED AT LOW			
CC	LEVELS. ISOFORM 4 IS EXPRESSED EXCLUSIVELY IN VOMERONASAL ORGAN.			
CC	-1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRECP			
CC	SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 3 ANK REPEATS.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
CC	EMBL: AF111108; AAD17196.1; -			
DR	EMBL: AF111107; AAD17195.1; -			
DR	EMBL: AF230803; AAG29951.1; -			
DR	EMBL: AF230802; AAG29950.1; -			
DR	MGI:109527; Trp2.			

P19838 homo sapien  
P54282 rattus norv  
Q04721 homo sapien  
Q35516 mus musculu  
Q9hcf6 homo sapien  
Q95271 homo sapien  
P97445 mus musculu  
Q9y566 homo sapien  
P57078 homo sapien  
Q07008 rattus norv  
Q02357 mus musculu  
P16157 homo sapien

DR InterPro: IPR002110; ANK.  
DR InterPro: IPR002111; Cat\_channel\_trpl.  
DR InterPro: IPR000636; M+channel\_nlg.  
DR InterPro: IPR002153; Trans\_recep.  
DR InterPro: IPR002706; Xrccl\_N.  
DR Pfam: PF00520; ion\_trans; 1.  
DR Pfam: PF01834; XRCCL\_N; 1.  
DR PRINTS: PR01097; TRNSRECEPTR.  
DR ProDom: PD023136; Xrccl\_N; 1.  
DR SMART: SM00248; ANK; 1.  
DR PROSITE: PS00088; ANK\_REPEAT; FALSE\_NEG.  
DR PROSITE: PS0297; ANK\_REPEAT\_REGION; FALSE\_NEG.  
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
KW ANK repeat; Repeat; Alternative splicing.  
FT DOMAIN 1 659 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 660 702 POTENTIAL.  
FT DOMAIN 681 702 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 703 723 POTENTIAL.  
FT DOMAIN 724 738 POTENTIAL.  
FT TRANSSEM 739 759 POTENTIAL.  
FT DOMAIN 760 789 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 790 810 POTENTIAL.  
FT DOMAIN 811 833 POTENTIAL.  
FT TRANSSEM 834 854 POTENTIAL.  
FT DOMAIN 855 899 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 900 920 POTENTIAL.  
FT DOMAIN 921 1172 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 301 330 ANK 1.  
FT REPEAT 377 406 ANK 2.  
FT REPEAT 430 459 ANK 3.  
FT DOMAIN 1140 1143 POLY-SER.  
FT VARSPLIC 1 111  
FT MLMSRTDSKSGKNSRVMFKDGFITPASGESWDRLRITC  
FT SPTFTRHQSFLAFLVRSSLSGLADVPVDPSPAGSGSLNQ  
FT NSTDVLESOPRPLWLTNPSTIRRTFFPDPT -> MGTKTHV  
FT VPW (IN ISOFORM 2).  
FT MISSING (IN ISOFORM 4).  
FT MISSING (IN ISOFORM 3).  
FT LVPK -> DPLS (IN ISOFORM 4).  
FT R -> K (IN REF. 2).  
FT S -> F (IN REF. 2).  
FT CONFLICT 633 653 Q -> R (IN REF. 2).  
FT CONFLICT 653 653 C -> Y (IN REF. 2).  
FT CONFLICT 774 774 T -> A (IN REF. 2).  
FT CONFLICT 797 797 L -> P (IN REF. 2).  
FT CONFLICT 1161 1161 L -> P (IN REF. 2).  
FT SEQUENCE -1172 AA; 130467 MW; B6A6F4BB941E946 CRC64;  
Query Match 4.0%; Score 182; DB 1; Length 1172;  
Best Local Similarity 19.1%; Pred. No. 0.00043;  
Matches 189; Conservative 120; Mismatches 350; Indels 332; Gaps 40;  
QY 8 PRAGGEVAELPGD---ESGTPGGEAFPLSSLA-----NLFEGEDGSLSPSPA 52  
DB 109 POTSREISELKMQLQLOFGLGRARMVLSAARKAPASVVSNNSHGPGC---PSRA 165  
QY 53 DASRPAGDGRNLRMKQGAERKGVNPDIDLESTLYESSVVGPKAPMDSLFYDGT 112  
DB 166 ESHEPRAE---EPNRTAVGRRRKRVQEP-----RRSLNSSSQPNRRGRT-----R 211  
QY 113 YRHSSDNKRWKKI-----IEKQSPKAPAPQPPPIKLVFNRPILFDIV 158  
DB 212 QROHRPOTKSDGCVQAAGCPICAGFFSTETLPQHAATCGESPPP----- 257  
QY 159 SRGSTADLGLPLFLTHKKRLT-----DEEFREPST-----OKTCL 195  
DB 258 QPASASLSSSESVLRHRRHVALTPVLPVKPQPNWTEIVNKKLKFPTLLRAIQEGQLG 317  
QY 196 PRALLNLSGRNDTIP-----VLLDIAERTGN-----WREFINSPFRD 233  
DB 318 VOOLLESSDASGAGPGPLRNVESEDRSWREALNLRGLGHEVITDVLNANVKDFDRQ 377  
QY 234 IYRGOTALHIAIERCKKHVELLVA-----QCADVHAQARG--RFQKDEGQGYFYFGE 287  
DB 378 IH-----EALLVAVDTHQPAVRRLLARLEREKGRKVDTKSFLAFFDSSIDGSRFAPGV 433

QY 288 PLSLAACNPHIVNYLTENPHKKADMRRODSRGNTVYLHALVAIADNTRENTKFTWKYD 347  
DB 434 PLTLACQKDLYEIAQLLMDQGHITA-----RHPVSCACLECSNARR-----YD 477  
QY 348 LLLLKCARLPDSNLEAVLANDGLSPMLMAAKTGKIGIFQHIIRREVTDDETRHLSRKF 407  
DB 478 LKFLSLSRI---NTYRGIASRAHLS---LASEDAMLAAFO--LSREL-----RRLARKEP 524  
QY 408 DWAYGPVYSSL-----YDLSSLDTC---GEEASVLEILVYNSKIENRHEMLA---VEPI 455  
DB 525 E--FKQYIALESQCQDYGFELLCMCNQNQSEVTAVNDLGEDSETEPEAGLQCAFEG 582  
QY 456 NEILLRDK-----VSYINVVSYLCAWVI-----FLTAYYQPLEGTPPYR 503  
DB 583 PNLARLRVAVNMQFOVAHPICQVQLSSIWCGNLGWRGSGTTIWRFLVASLFLTMPFL 642  
QY 469 -----VSFYINVVSYLCAWVI-----FLTAYYQPLEGTPPYR 503  
DB 643 CIGYWLAPKSQLGRLLKIPVKFLLHSASYLWFLFLGSLVMTQSLTFKGRSOSVWE 702  
QY 504 TTVLYRLAGEVITLFTGVLFFTTNKIDLPKMKCPGVNSLFDIGSFQLLFYIYSLVIVS 563  
DB 703 TSLHMIWVG-----FLMECKEYVIE---GLRSYLLDW-----WNFLDQVI 741  
QY 564 AALYLAGI-----EAYLAVVWVFL--V 583  
DB 742 LSLYLASFALRLLLAGLAVMHCDA SDSTTCRCFTTAERSEWRTDPOFLAEVLFTVSM 801  
QY 584 LGHMNALYTRGLKLTGTSYIMIOKILFKDLRFLLVLLFMIGYASALVSLNLANPCANMK 643  
DB 802 LSFTRLAYILPAHESLGTLQISIGKMI--DDMIRFMFLMIILTAFLCGL----- 849  
QY 644 VCNEDOTNCTVPTPSCROSETSTFLDLFLKLTIGMDLEMLSSTKYPVVFILLVTVI 703  
DB 850 -----NNIYVP--YQSEKLGNFNETFQFLFTWFMGMEHTVVYDMQFLVPEVGRAMY 902  
QY 704 ILTFVL---LLNMLIALMGETVQVSKSHIWKLOWATILDIR---SFPV----- 750  
DB 903 IFTVMVIVLLNMLIAMITNSFOKIEDDADVENKFAKSKLYLSYFREGTLTPVPFNLPS 962  
QY 751 -----FLRKAFR---SGEMVTYVGSKSDGTP 772  
DB 963 PKAAFYLVRIFRFLCCGSSCCAKKASDIPP 993  
RESULT 2  
TRP7\_HUMAN STANDARD; PRT; 862 AA.  
ID TRP7\_HUMAN  
AC QHGX4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Short transient receptor potential channel 7 (TrpC7) (TrpC7 protein).  
GN TRPC7 OR TRP7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Murphy C.T., Li S., Jordan N.J., Reaves B.J., Wolstenholme A.J.,  
RT "Distribution of a novel human capacitative calcium entry channel;  
RT htrp7".  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. ACTIVATED BY  
CC DIACYLGLYCEROL (DAG) (BY SIMILARITY). MAY ALSO BE ACTIVATED BY  
CC INTRACELLULAR CALCIUM STORE DEPLETION.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -|- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC  
 CC SUBFAMILY.  
 CC -|- SIMILARITY: CONTAINS 4 ANK REPEATS.  
 CC  
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 CC  
 CC EMBL: AJ272034; CAC03489.1; -  
 CC InterPro: IPR002110; ANK.  
 CC InterPro: IPR002111; Cat\_channel\_TrpL.  
 CC InterPro: IPR000636; M+channel\_nlg.  
 CC InterPro: IPR002153; Trans\_recep.  
 CC InterPro: IPR004729; Trp\_CaChannel.  
 CC Pfam: PF00023; ank; 3.  
 CC Pfam: PF00520; ion\_trans; 1.  
 CC PRINTS: PR01097; TRNSRECEPTR.  
 CC SMART: SM00248; ANK; 3.  
 CC TIGRFAMS: TIGR00870; trp; 1.  
 CC PROSITE: PS50088; ANK\_REPEAT; FALSE\_NEG.  
 CC PROSITE: PS0297; ANK\_REPEAT\_REGION; FALSE\_NEG.  
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 KW ANK repeat; Repeat; Glycoprotein.  
 FT DOMAIN 1 351  
 FT TRANSMEM 352 372 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 373 383 POTENTIAL.  
 FT TRANSMEM 384 404 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 405 465 POTENTIAL.  
 FT TRANSMEM 466 486 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 487 537 POTENTIAL.  
 FT TRANSMEM 538 558 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 559 581 POTENTIAL.  
 FT TRANSMEM 582 602 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 603 651 POTENTIAL.  
 FT TRANSMEM 652 672 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 673 862 POTENTIAL.  
 FT REPEAT 42 71 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 77 106 ANK 1.  
 FT REPEAT 108 134 ANK 2.  
 FT REPEAT 163 192 ANK 3.  
 FT CARBOHYD 514 514 N-LINKED (GLCNAC, ...) (POTENTIAL).  
 SQ SEQUENCE 862 AA; 99561 MW; C516E59E80AEF4B0 CRC64;  
 Query Match 4.0%; Score 181.5; DB 1; Length 862;  
 Best Local Similarity 20.3%; Pred. No. 0.0003;  
 Matches 149; Conservative 106; Mismatches 250; Indels 229; Gaps 36;  
 QY 185 FREPSTGKTLCPKALLNLNSGRNDTIPVLLDIAERTGNRRFINSFRRDIYRGOTALHI 244  
 DB 33 FNEKGSLF--PEERFELDSAEYGNIPVVRKMLESKTLN-----FNCVDYMGQNALQL 84  
 QY 245 AIERRCKHYVELLV-----AOG-----ADVHA 266  
 DB 85 AVGNHELVTELLKKENLARVDGALLAISKGYYRIVEAILNHPAFAOGRLTLSPLEQ 144  
 QY 267 QARGRFQPKDGGYFYFGL-PLSLAAGTNPVHNYL-----TENPH-----KKA 312  
 DB 145 ELRDDDFAYDEGDTGRFSDHTPTILAAHCQEYIEVHILLKRGARTERPHDYFCCKNECT 204  
 QY 313 DMRRDD--SRGNTVHLVAIADNTRNTKFTVKYVDLL--KCARLPDSDNLEAVLAN 368  
 DB 205 EKQRDSFHSRNRNAYKGLASAYLSLSSDDPVLTALELSNEARL---ANIETFFKN 261  
 QY 369 DGLSLPMAAKTGKIGIFOHIRREVTDEDTRHLSKFKDWA--YGPVYSSL-----YDL 421  
 DB 262 D-YRLSMOCKDFVVGVD-LCRDTEEEVAILNGVDNFOVSDHHRPSLSRLKLAKEYV 319  
 QY 422 SSL---DTGGEASVLEILVYNSKIENRHEMLAVE-----PINE 457

DB 320 KKEVAHPNCOQQ---LLTMWYENLSGLRQOSIAVFLAVFGVSGIGLFFLAIAIYWIAPCSK 376  
 QY 458 L---LRDKWRKF--GAVSYFVNVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTVTDVLRLA 512  
 DB 377 LGRTLRSPWKFVAHAVSTI---FLGLLVVNASDRF---EGVKTLPNETTDPKQI 428  
 QY 513 GEVITLFTGVLFPTNIKOLFMK-----KCP-----GVNSLF 544  
 DB 429 FRVKT---TQPSWTEM--LIMKWGLMIWSECKEIEWEGPREVVLHLNLLDFGMLSF 482  
 QY 545 IDGSF-----QLLYFIY-----SVLVISA 564  
 DB 483 V-ASFTARFMAFLKATEAQLYDQHQDDTLHNVSPLPPEYAYTARDKWPSPDQIISE 541  
 QY 565 ALVLAGEIAYLAVMVFALVGLGMNALYFTRGLKLTGYTIMIKILFKDLFRELLVLLF 624  
 DB 542 GLY-----AJAVLSFSRIAYILPANESFGLQISLQRTV-KDIFKFWVIFIMV 589  
 QY 625 MIGYASALVSLNPNCAVMKVCNEDQNTCTVPTVPSCRDSETFSTFLDLFKLTIGMDLE 684  
 DB 590 FVAF--MIGMFNLVSYRGAKYNPAFTV-----EESFKTLFWSIFGLS-----E 632  
 QY 685 MLSST-KYPVVF-----ILLVYIILTFVLLNMLIALMGETVGOVSKESKHIWKLQWA 738  
 DB 633 VISVLYKDHKFTENIGYVLYGVYNTVMVYVLLNMLIAMINNSYQIEEDADVWKFA 692  
 QY 739 ---TTILDIERSP 749  
 DB 693 KLWLSYFDEGRITLP 706  
 RESULT 3  
 TRP7\_MOUSE STANDARD; PRT; 862 AA.  
 AC Q9WVC5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Short transient receptor potential channel 7 (TrpC7) (mTRP7).  
 GN TRPC7 OR TRPP8 OR TRP7.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99419008; PubMed=10489066;  
 RA Okada T., Inoue R., Yamazaki K., Maeda A., Kurosaki T., Yamakuni T.,  
 RA Tanaka I., Shimizu S., Ikenaka K., Imoto K., Mori Y.;  
 RT "Molecular and functional characterization of a novel mouse transient  
 RT receptor potential protein homologue TRP7, Ca(2+)-permeable cation  
 RT channel that is constitutively activated and enhanced by stimulation  
 RT of G protein-coupled receptor.";  
 RL J. Biol. Chem. 274:27359-27370(1999).  
 CC -|- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. ACTIVATED BY  
 CC DIACYLGLYCEROL (DAG). MAY ALSO BE ACTIVATED BY INTRACELLULAR  
 CC CALCIUM STORE DEPLETION.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -|- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC  
 CC SUBFAMILY.  
 CC -|- SIMILARITY: CONTAINS 5 ANK REPEATS.  
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CC EMBL; AF139923; AAD42069.1; -
DR MGD; MGI:1349470; Trp8.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; M-channel_nlg.
DR InterPro; IPR002153; Trans_recep.
DR InterPro; IPR004729; Trp_CaChannel.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01097; TRNSRECEPTR.
DR SMART; SM00248; ANK; 1.
DR TIGRfams; TIGR00870; trp; 1.
DR PROSITE; PS00088; ANK_REPEAT; FALSE_NEG.
DR PROSITE; PS00297; ANK_REPEAT_REGION; FALSE_NEG.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Glycoprotein.
FT DOMAIN 1 351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 352 372 POTENTIAL.
FT DOMAIN 373 383 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 384 404 POTENTIAL.
FT DOMAIN 405 465 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 466 486 POTENTIAL.
FT DOMAIN 487 537 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 538 558 POTENTIAL.
FT DOMAIN 559 581 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 582 602 POTENTIAL.
FT DOMAIN 603 651 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 652 672 POTENTIAL.
FT DOMAIN 673 862 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 71 ANK 1.
FT REPEAT 77 106 ANK 2.
FT REPEAT 108 134 ANK 3.
FT REPEAT 163 192 ANK 4.
FT REPEAT 563 592 ANK 5.
FT CARBOHYD 514 514 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 862 AA; 99474 MW; C2E2CE1A6A9FC3D CRC64;

Query Match
Best Local Similarity 3.98; Score 178.5; DB 1; Length 862;
Matches 146; Conservative 105; Mismatches 258; Indels 221; Gaps 33;

QY 185 FRPSTKTKLPRALLNLSNGRNDTIPVLDIAERTGNMREFNSPRDIYRGQTALHI 244
DB 33 FNEKGTSLT--PEERELDAEYGNIPVVRKMLEESKTLN-----FNCVDYMGQNALQL 84
QY 245 AIERRCKHYVELLV-----AOG-----ADVHA 266
DB 85 AVGNEHLEVTLELLKKNLARVGDALLAISKGVVRIVEAILSHPAFAQORLTLSPLEQ 144
QY 267 QARGRFQPKDEGGYFYFGEI-PLSLAACTNQHIVNVL-----TENPH-----KKA 312
DB 145 ELRDDDFAYDEGDTRESDHITPILAAHCQVEIVHILLKGARIEPHDYCKCNECT 204
QY 313 DMRRQD---SRGNTVHLVAIAONTRENTKFTKMYDLLLL--KCARLFPDSNLEAVLNN 368
DB 205 EKORKDSFSHRSMNAYKGLASAAVLSLSEDPVLTALSNEIARL---ANITETFEKN 261
QY 369 DGLSPLMMAKTGKIGIF-----QHIIREV-----TDSDTHLSR-----KFK 407
DB 262 D-YRKLVSQCKDFVGVLDLCRDETEVEAILNGDVLNQVSDHRRPSLSRIKAIKVEVK 320
QY 408 DWAYGP-----VYSSLYDLSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEL 458
DB 321 KFAVHPNCQOQLTMVYENLSGLRQOSIAVKFLAVFGVSGLFLATAYWIAFCSKLGQT 380
QY 459 LRDKWRKF--GAVSFYINNVSYLCAMVIFTLTAYOPELGTPPYRTTVDYLRAGEVI 516
DB 381 LRSPFMKFAVAHVSFTI---FLGLLVNNSDRF---EGVKTLPLNETFDYKQIPRVK 432
QY 517 TLETGVLFFFTNIKDLFMK-----KCP-----GVNSLFDGS 548
DB 433 T-----TQFSWTEM--LIMKWVLGMWSECKEIVEGPREYVLHNLNLLDFGMLSFV-AS 485

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QY 549 F-----QLLYFYI-----SVLVIVSAALYL 568
DB 486 FTAREMAFLKASEAQLVVDVQVDTLHNVSLPEVAYFTYARDKWPSPDQIISEGLY- 544
QY 569 AGIAYLAVVAVFVLVGLWMNALYFTRGLKLTGYTSIMQIKLFDKDLFRLLVYLLFMIGY 628
DB 545 -----AIAVLSFSRIAYILPANESFGPLQISLGRTV-KDIFKFWIFIMVFAV 593
QY 629 ASALVSLNPNCAKMKVCNEDQTNCTVPTPSCRDSEFTFLLDLFLKLTIGMGDLEMLSS 688
DB 594 ---WIGMFLSYRGAKYNPAFTV-----EESFKTLFWSIFGLS-----EIVSV 636
QY 689 T-KYPVVI-----ILVTYIILTFVLLNNLIALMGETGVQVSKESKHVQLQWA---T 739
DB 637 VLKYDHKFIENIGVLYGVYNTVMVTVLLNNLMIANNINSYQETIEDADVEWKFARAKLWL 696
QY 740 TILDIERSP 749
DB 697 SYFDEGRTLP 706

RESULT 4
TRP2_RAT
ID TRP2_RAT STANDARD; PRT; 885 AA.
AC Q9R283;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 2 (TrpC2) (rTRP2).
GN TRP2 OR TRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99254120; PubMed=10318963;
RA Liman E.R., Corey D.P., Dulac C.;
RT "TRP2: a candidate transduction channel for mammalian pheromone
RT sensory signaling.";
RL Proc Natl Acad Sci U S A. 96:5791-5796(1999).
CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED CALCIUM PERMEANT
CC CATION CHANNEL. PROBABLY IS OPERATED BY A PHOSPHATIDYLINOSITOL
CC SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR
CC G-PROTEIN COUPLED RECEPTORS. IS NOT ACTIVATED BY INTRACELLULAR
CC CALCIUM STORE DEPLETION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN VOMERONASAL ORGAN
CC NEURONS (SENSORY MICROVILLI).
CC -!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF136401; AAD31453.1; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; M-channel_nlg.
DR InterPro; IPR002153; Trans_recep.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01097; TRNSRECEPTR.
DR SMART; SM00248; ANK; 1.
DR PROSITE; PS00088; ANK_REPEAT; FALSE_NEG.
DR PROSITE; PS00297; ANK_REPEAT_REGION; FALSE_NEG.

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DR InterPro: IPR004729; Trp\_CaChannel.  
 DR Pfam: PF00023; ank; 2.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR PRINTS: PR01097; TRNSRECEPTR.  
 DR SMART: SMO0248; ANK; 2.  
 DR TIGRFAMs: TIGR00870; trp; 1.  
 DR PROSITE: PS50088; ANK\_REPEAT; 1.  
 DR PROSITE: PS50297; ANK\_REPEAT; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 KW ANK repeat; Repeat; Alternative splicing.  
 FT DOMAIN 1 331 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 332 352 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 353 364 POTENTIAL.  
 FT TRANSMEM 365 385 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 386 438 POTENTIAL.  
 FT TRANSMEM 439 459 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 460 471 POTENTIAL.  
 FT TRANSMEM 472 492 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 493 513 POTENTIAL.  
 FT TRANSMEM 514 534 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 535 601 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 602 622 POTENTIAL.  
 FT DOMAIN 623 981 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 71 100 ANK 1.  
 FT REPEAT 143 172 ANK 2.  
 FT DOMAIN 617 981 BINDS TO ITPR1, ITPR2 AND ITPR3 (BY SIMILARITY).  
 FT SITE 979 981 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN (BY SIMILARITY).  
 FT VARSPLIC 1 513 MISSING (IN ISOFORM BETA).  
 FT SEQUENCE 981 AA; 112531 MW; 57B172FD65B791C9 CRC64;  
 Query Match 3.6%; Score 166; DB 1; Length 981;  
 Best Local Similarity 19.7%; Pred. No. 0.0037;  
 Matches 139; Conservative 102; Mismatches 203; Indels 262; Gaps 34;  
 QY 222 NMRFE-----INSFPRD-----IYY 236  
 DB 2 NMAQYKRNVDYRIPRIVRAESELSPSEKAYLNAVEKGDYASVKKSLSEAEIYF 61  
 QY 237 R-----GOTALHIAERRCKHYVELLAQADV-----HA 266  
 DB 62 KINICIDPLGRALTALAIENENLELIELLSFNYYVDALLHAIRKEVVGAVELLNKH 121  
 QY 267 QARGRFQPK---DEGYFTFGEI-----PLSLAAGTQPHVNYLFE-----NPKHKA 312  
 DB 122 KPSEKQVPPILLDK---QFSEFTPDITPIILAAHTNNVEIILKLVQKGVSVPRPH--- 174  
 QY 313 DMRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLLKCARLPDSNLEAVLNNDG-L 371  
 DB 175 -----EVRNCVCEVSSDVSLSRHSR-----RLNIYKALASPSLIALSSDPFL 220  
 QY 372 SPLMMAAKTGKIGIFQHIIRREVTEDTRHLSRKFQDWYGV-----PVYSLYD 420  
 DB 221 TAFQLSWELQELSKVNEFESEYEE-----LSRQCKQFAKDLDDOTRSSRELEILNYRD 275  
 QY 421 LSSL--DTCGEASVLEILY-YNSKIENRHEMLAVEPINELLRKW-----RKFGAV 469  
 DB 276 DNSLLEROSGNDLARKLAIKYROK-----EFVAQPCQQLASRWYDEFGWRRRHWAV 330  
 QY 470 -----SFYINVSYLCAWIFTLTAYY--- 491  
 DB 331 KWTCTFVGLLFPVFSVCYLIAPKSPGLGFIKPFKIFKHTASYLTFLELLLSAOSHID 390  
 QY 492 ---QPLEGTTPPYRTVDYLRLA-----GEVITLGTGVLFFFT-----NIKDLFMKKC 537  
 DB 391 RSDLNROGPPP---TIVENMILPWLGFIWGEIKOMWGLQDYIDHWNLMDVFM--- 443  
 QY 538 PGVNSLIDG-SQLLYFI-YSVI-----VTVSAALY-LAGIEAYLAWVVALV 583  
 DB 444 ---NSLYLATISKIVAFVKYSALNPRESMDWHMPTLVAEALFAIANIFSSRLISL--- 497  
 QY 584 LGMNALLYFRGLKLTCTYSIMIOKILFKDLFRFLLYLLFMICYASALVSLNPPCANMK 643

DB 498 -----FTANSHL-GPLQISLGRMEL-DILKELFIYCLVLLAFANGLNQLYFYETK 547  
 QY 644 VCNEQDQNTCTVPTSPCRDSETFSTF-----LLDLFKLTICMGDL-----EMLSS 688  
 DB 548 GLSCCKGIRCE-----KQNAFSTLFTLOSLSFWSIFGLNLYVTVNVAOHEFTFVGA 600  
 QY 689 TKYPVFIILLVTVIILFVLLNMLALMGETVQGVSKSKHWWK 734  
 DB 601 TMFG-----TYNVISLVLLNMLIAMMNSYQLIADHADIEMK 638  
 RESULT 6  
 TRP4\_MOUSE  
 ID TRP4\_MOUSE STANDARD; PRT; 974 AA.  
 AC Q90UQ5; Q90ZC0; Q90UQ9; Q62350;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Short transient receptor potential channel 4 (TrpC4) (Receptor-activated cation channel TRP4) (Capacitative calcium entry channel Trp4).  
 GN TRPC4 OR TRRP4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC TISSUE=Brain;  
 RA Zhu X., Boulay G., Jiang M., Birnbaumer L.;  
 RT "Trp4 is involved in capacitative calcium entry in murine cells."  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RA Qian F., Philipson L.H.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC TISSUE=Brain;  
 RA Morl Y., Takada N., Okada T., Wakamori M., Imoto K., Wanifuchi H., Oka H., Oba A., Ikenaka K., Kurosaki T.;  
 RT "Differential distribution of TRP Ca2+ channel isoforms in mouse brain."  
 RL NeuroReport 9:507-515(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=20545496; PubMed=10980202;  
 RA Tang Y., Tang J., Chen Z., Trost C., Flockerzi V., Li M., Ramesh V., Zhu M.X.;  
 RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ domain-containing protein, NHERF."  
 RL J. Biol. Chem. 275:37559-37564(2000).  
 RN [5]  
 RP SEQUENCE OF 505-642 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=96003894; PubMed=7575478;  
 RA Petersen C.C.H., Berridge M.J., Borge M.F., Bennett D.L.;  
 RT "Putative capacitative calcium entry channels: expression of Drosophila trp and evidence for the existence of vertebrate homologues."  
 RL Biochem. J. 311:41-44(1995).  
 RN [6]  
 RP FUNCTION.  
 RX MEDLINE=21113116; PubMed=11175743;  
 RA Freichel M., Suh S.H., Pfeifer A., Schweig U., Trost C., Weissgerber P., Biet M., Philipp S., Freise D., Droogmans G., Hofmann F., Flockerzi V., Nilius B.;  
 RT "Lack of an endothelial store-operated Ca2+ current impairs agonist-dependent vasorelaxation in TRP4-/- mice."  
 RL Nat. Cell Biol. 3:121-127(2001).  
 CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE



RA Juengling E., Luckhoff A., Putney J.W. Jr.;  
 RT "Cloning and expression of the human transient receptor potential 4  
 RT (TRP4) gene: localization and functional expression of human TRP4 and  
 RT TRP3.";  
 RL Biochem. J. 351:735-746(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; DELTA AND GAMMA).  
 RC TISSUE=Embryonic kidney;  
 RX MEDLINE=21099836; PubMed=11163362;  
 RA Mery L., Magnino F., Schmidt K., Krause K.-H., Dufour J.-F.;  
 RT "Alternative splice variants of htrp4 differentially interact with the  
 RT C-terminal portion of the inositol 1,4,5-trisphosphate receptors.";  
 RL FEBS Lett. 487:377-383(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=21671347; PubMed=11713258;  
 RA Schaefer M., Plant T.D., Stresow N., Albrecht N., Schultz G.;  
 RT "Functional differences between TRPC4 splice variants.";  
 RL J. Biol. Chem. 277:3752-3759(2002).  
 RN [4]  
 RP SEQUENCE OF 514-633 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=96234226; PubMed=8646775;  
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,  
 RA Birnbaumer L.;  
 RT "trp, a novel mammalian gene family essential for agonist-activated  
 RT capacitative Ca<sup>2+</sup> entry.";  
 RL Cell 85:661-671(1996).  
 CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN  
 CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE  
 CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.  
 CC -1- SUBUNIT: ISOFORM ALPHA BUT ISOFORM BETA ASSOCIATES WITH INOSITOL-  
 CC 1,4,5-TRIPHOSPHATE RECEPTOR (ITPR). INTERACTS WITH NHERF (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA (SHOWN HERE), BETA, DELTA  
 CC AND GAMMA; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PLACENTA. EXPRESSED AT  
 CC LOWER LEVELS IN HEART, PANCREAS, KIDNEY AND BRAIN. ISOFORM ALPHA  
 CC WAS FOUND TO BE THE PREDOMINANT ISOFORM. ISOFORM BETA WAS NOT  
 CC FOUND IN PANCREAS AND BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: AF063822; AAF22927.1; -  
 DR EMBL: AF063823; AAF22928.1; -  
 DR EMBL: AF063824; AAF22929.1; -  
 DR EMBL: AF063825; AAF22930.1; -  
 DR EMBL: AF175406; AAD51736.1; -  
 DR EMBL: AF421358; AAL24549.1; -  
 DR EMBL: AF421359; AAL24550.1; -  
 DR EMBL: U40983; AAC50630.1; -  
 DR Genew: HGNC:12336; TRPC4.  
 DR MIM: 603651;  
 DR InterPro: IPR002110; ANK.  
 DR InterPro: IPR002111; Cat\_channel\_TrpL.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR002153; Trans\_recep.  
 DR InterPro: IPR004729; Trp\_CaChannel.  
 DR Pfam: PF000023; ank; 2.  
 DR Pfam: PF00520; ion\_trans; 1.

DR PRINTS: PRO1097; TRNSRECEPTRP.  
 DR SMART; SM00248; ANK; 2.  
 DR TIGRFAMS; TIGR00870; trp; 1.  
 DR PROSITE; PS00088; ANK\_REPEAT; 1.  
 DR PROSITE; PS0297; ANK\_REPEAT; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 KW ANK repeat; Repeat; Alternative splicing.  
 FT DOMAIN 1 329 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 330 350 POTENTIAL.  
 FT DOMAIN 351 362 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 363 383 POTENTIAL.  
 FT DOMAIN 384 436 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 437 457 POTENTIAL.  
 FT DOMAIN 458 469 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 470 490 POTENTIAL.  
 FT DOMAIN 491 511 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 512 532 POTENTIAL.  
 FT DOMAIN 533 599 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 600 620 POTENTIAL.  
 FT DOMAIN 621 977 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 69 98 ANK 1.  
 FT REPEAT 141 170 ANK 2.  
 FT DOMAIN 377 382 POLY-LEU.  
 FT DOMAIN 615 977 BINDS TO ITPR1, ITPR2 AND ITPR3.  
 FT SITE 972 977 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN  
 FT VARSPLIC 629 693 MISSING (IN ISOFORM GAMMA).  
 FT VARSPLIC 730 870 MISSING (IN ISOFORM DELTA).  
 FT VARSPLIC 785 868 MISSING (IN ISOFORM BETA AND ISOFORM  
 FT GAMMA).  
 SQ SEQUENCE 977 AA; 112100 MW; 77E4D27C374D660E CRC64;  
 Query Match 3.6%; Score 164; DB 1; Length 977;  
 Best Local Similarity 20.4%; Pred. No. 0.005;  
 Matches 143; Conservative 103; Mismatches 214; Indels 242; Gaps 34;  
 QY 201 NLSNGRNDIPVLLDIAER--TGNMREFINSPPR-----DIYR----- 237  
 DB 9 NYNAPYDRIPLRIVRAESELSPSEKAYLNAVEKGDYASYVKSLEAEIYFKINICIDP 68  
 QY 238 -GQTALHIAIERCKHYVELLVAQADV-----HAQARGFP 275  
 DB 69 LGRTALLIAIENENLELIELLSFNVYVGDALLHAIRKEVGVAGVELLHNHKKPSGKQVP 128  
 QY 276 K--DEGGYFYFGEI-----PLSLAACTNQPHIVNYLTE-----NPHKKADMRRODSRG 321  
 DB 129 PILLDK---QFSEFTDITPILAAHTNNYEIKLLVQGVSVPRPH-----EVRC 176  
 QY 322 NTVLHALVAIADNTRNTKFKWYDILLKCARLPDNLNLEAVLNNDG-LSPMLMAAKT 380  
 DB 177 NCVECVSSSDVDSLRHSR-----RLNIYKALASPSLIALSSEDPFLTAFLSWEL 227  
 QY 381 KGIGIFQHIIRREVTDTRHLRSKFKDWAYGPVSSLYDLSLDCTCGEASVLEILVY- 439  
 DB 228 QELSKVENEKSEYEE-----LSRCKQFA-----KDL-LDQTRSRELEIILNR 272  
 QY 440 --NSKIE-----NRHEMLAVEFINELLRDKW-----RKFGV----- 469  
 DB 273 DONSLIEQSGNDLRLKLAIRKQEFVAQPCQQLASRWYDEFPGRWRHWAVMVMT 332  
 QY 470 -----SFYINVSYLCAMVIFTLTAY-----Q 492  
 DB 333 CFTIGLLFPVSVCYLIAKPSPLGLFIRKPFKIFCTASYLTFTLELLLASDHDRSDL 392  
 QY 493 PLEGTPPYRTVDYLRLA-----GEVITLFTGVLFFFT-----NIKDLFMKKCPGVN 541  
 DB 393 NRQGGPP-----TIVEMWILPWLVGFINGEIKQMDGLQDYIHDWNLMDFVM-----N 442  
 QY 542 SLFIDG-SFOLLYFI-YSVL-----VIVSAALY-LAGIEAYLAWFALVGLWM 587  
 DB 443 SLYLATISLKIIVAFVKYSALNPRESMDMNHPTLVAELFAIANIFFSLLSL----- 495  
 QY 588 NALYFTRGLKLTGYSIMIQKILFKDLFRFLLYVILFMIGYASALVSLNLPNCANKVCNE 647

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496 ----FTANSHL-GPQISLGRMLL-DILKFLFIYCLVLLAFANGLNOLY-----FYFE 542
QY 648 DOTNCTVTPSCRDSEFTSF---LLDLKFLITIGMDL-----EMLSSKYP 692
Db 543 ETGKLTGKIGICEKQNNAFSLFETLQSLFWSIFGLINLYVTNKAHQEFTEFGATMFG 602
QY 693 VVFILLVYIILFTVLLNNMLIAMGETVQGVSKESKHIMK 734
Db 603 -----TYNVISLVLLNNMLIAMMNSYQIADHADIEWK 636

RESULT 8
TRP4_RAT
ID TRP4_RAT STANDARD: PRT; 977 AA.
AC O35119; O9EO75; O9EO74;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 4 (TrpC4) (Trp4)
DE (Capacitative calcium entry channel 1) (CCE1).
GN TRPC4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC STRAIN=Wistar Inamichi; TISSUE=Brain;
RX MEDLINE=97189270; PubMed=9037541;
RA Funayama M., Goto K., Kondo H.;
RT "Cloning and expression localization of cDNA for rat homolog of TRP
RL protein, a possible store-operated calcium (Ca2+) channel.";
RN Brain Res. Mol. Brain Res. 43:259-266(1996).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=20545496; PubMed=10980202;
RA Tang Y., Tang J., Chen Z., Trost C., Flockerzi V., Li M., Ramesh V.,
RA Zhu M.X.;
RT "Association of mammalian Trp4 and phospholipase C isozymes with a PDZ
RL domain-containing protein, NHERF.";
J. Biol. Chem. 275:37559-37564(2000).
CC -1- FUNCTION: THOUGHT TO FORM NON-SELECTIVE A RECEPTOR-ACTIVATED
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: ISOFORM ALPHA BUT NOT ISOFORM BETA ASSOCIATES WITH
CC INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (ITPR). INTERACTS WITH NHERF
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC -----
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CC -----
CC EMBL; AB008889; BAA23599.1;
CC DR EMBL; AF288407; AAC21809.1;
CC DR EMBL; AF288408; AAC21810.1;
CC DR InterPro; IPR002110; ANK.
CC DR InterPro; IPR002111; Cat_channel_TrpL.
CC DR InterPro; IPR000636; M+channel_nlg.

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DR InterPro; IPR002153; Trans_recep.
DR InterPro; IPR004729; Trp_CaChannel.
DR Pfam; PF00023; ank. 2.
DR Pfam; PF00520; ion_trans. 1.
DR PRINTS; PR01097; TRNSRECEPTR.
DR SMART; SMO0248; ANK. 2.
DR TIGRFAMS; TIGR00870; trp. 1.
DR PROSITE; PS50088; ANK_REPEAT. 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION. 1.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Alternative splicing.
FT DOMAIN 1 329 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 330 350 POTENTIAL.
FT DOMAIN 351 362 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 363 383 POTENTIAL.
FT DOMAIN 384 436 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 437 457 POTENTIAL.
FT DOMAIN 458 469 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 470 490 POTENTIAL.
FT DOMAIN 491 511 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 512 532 POTENTIAL.
FT DOMAIN 533 599 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 600 620 POTENTIAL.
FT DOMAIN 621 974 CYTOPLASMIC (POTENTIAL).
FT REPEAT 69 98 ANK 1.
FT REPEAT 141 170 ANK 2.
FT DOMAIN 615 977 BINDS TO ITPR1, ITPR2 AND ITPR3 (BY
FT SIMILARITY).
FT SITE 975 977 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN
FT VARSPLIC 784 867 MISSING (IN ISOFORM BETA).
FT CONFLICT 11 11 N -> D (IN REF. 1).
FT CONFLICT 72 76 TALLI -> GLFSL (IN REF. 1).
FT CONFLICT 121 135 PSGEKQVPPILLDKQ -> AQRREAGASHPPWQT (IN
FT REF. 1).
FT CONFLICT 204 204 A -> G (IN REF. 1).
FT CONFLICT 385 411 OHIDRSLNROGPPPTIVEMWILPVL -> STST (IN
FT REF. 1).
FT CONFLICT 681 681 K -> M (IN REF. 1).
FT CONFLICT 705 705 Q -> H (IN REF. 1).
FT CONFLICT 728 728 E -> D (IN REF. 1).
FT CONFLICT 807 807 A -> V (IN REF. 1).
FT CONFLICT 873 873 Q -> R (IN REF. 1).
FT CONFLICT 888 888 K -> Q (IN REF. 1).
FT CONFLICT 922 977 VGRVCSFKSEKVVVEDTVPIPKKHAQEDSSIDYDLS
FT PTTVAHEDYVTRFL -> GRQESVLLQLVGEGGWEDNR
FT YYTKRNPTRGDSKHKMI (IN REF. 1).
SQ SEQUENCE 977 AA; 11847 MW; 6F86DA95261E0ECD CRC64;

Query Match 3.5%; Score 161; DB 1; Length 977;
Best Local Similarity 20.6%; Pred. No. 0.0079;
Matches 143; Conservative 104; Mismatches 220; Indels 228; Gaps 34;

QY 201 NLNGRNDTIPVLLDIAER--TGNMREFINSFPR-----DIYR----- 237
Db 9 NVNAPYDRIPRLIVRAESELSPSEKAYLNAVEKGDYASKVKSLEAEIVFKINICIDP 68
QY 238 -GOTALHAIATERCKHVVVELLVAGADV-----HAQARGRFQP 275
Db 69 LGRTALLIATENENLEILLISFNVYVGDALLHAIKRVGVAVELLNHHKPSGEQVP 128
QY 276 K---DEGYVYFCEL-----PLSLAAGTNPHTVNYLITE-----NPHKADMRRDSRG 321
Db 129 PILLDK---QFSEFTPDTPPIILAHNTNVEIKLLVQKGVSPRPH-----EVRC 176
QY 322 NTVLHALVAIADTNTRENTKVTKMYDILLKLCARLFPDSNLEAVLNNDG--LSPLMMAKT 380
Db 177 NCVECVSSSDVSDLSRHS-----RLNIYKALASPSLIALSSSEDPeltaFQLSWEL 227
QY 381 GKIGIPQHIIRREVTDTHRLSRKFKDMAYGPVYSSLYDLSLDTGCGEASVLEILVY- 439
Db 228 QELSKVENEKFEVEE-----LSRQCKQFA-----KDL--LDOTRSSRELEILINR 272

```

QY 440 --NSKIE-----NPHEMLAVEPINELLRDKW-----RKFGAV-----469  
 Db 273 DNSSLIEQSGNDLRLAIAIKYRQKEFVAQPCOQLASRYDFFGRRRRHWAQMYT 332  
 QY 470 -----SFVINVSVYLCAMVITLTAY-----Q 492  
 Db 333 CFIIIGLLFPVSVYLIAPKPLGLFIRKPIKFKICHFTASVLTFLFLLLLASQHIDRSDL 392  
 QY 493 PLEGTTPPYPTVDVYRLA-----GEVITLFTGVLFFT-----NKKDLFMKKKPCGVN 541  
 Db 393 NRQGGPPP-----TIVEMILPWLGVINGEIKOMDGGQLQDIHOWNLMDVFM-----N 442  
 QY 542 SLFIDG-SFQLLYFI-YSVL-----VIYSAALY-LAGIAYLAVAVFALVLCWM 587  
 Db 443 SLIYATLSLKIVATVKVYSALNPRSDWMHPTLVAEALFAIANFSSURLISL-----495  
 QY 588 NALVFTGRLKLTGYYSIMIOIKFLKDFRFLVLLFMIGYASALVSLNPNCAKMKVCNE 647  
 Db 496 ----FTANSHL-GPLQISLGRMLL-DILKFLFIYCLVLLAFANGLNQLFYFEETKGLSC 549  
 QY 648 DOTNCTVPTPSCDSETFSTF---LLDLFKLTGMGDLEMSSTKYPVVF-----IILL 699  
 Db 550 KGIRCE-----KONNAFSTLFTLOSLEWISFGLINL-YVTNVKAQHEFTDFVGATMF 601  
 QY 700 VTYILTFVLLNLMLALMGETVGVQVSKSHIWK 734  
 Db 602 GTYNVISLVLLNLMLAMNNSYQIADHADIWK 636

## RESULT 9

TRL2\_HUMAN  
 ID TRL2\_HUMAN STANDARD; PRT: 1503 AA.  
 AC Q94759; Q96KN6;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Long transient receptor potential channel 2 (Ltrpc2) (Transient  
 DE receptor potential channel 7) (Trpc7).  
 GN TRPM2 OR LTRPC2 OR TRPC7 OR KNP3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=99026133; PubMed=9806837;  
 RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Asakawa S., Ito F.,  
 RA Shimizu N.;  
 RT "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7)  
 RT highly expressed in brain.";  
 RL Genomics 54:124-131(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Wehage E., Eisfeld J., Heiner I., Juengling E., Zitt C.,  
 RA Luckhoff A.;  
 RT "Splice variants of LTRPC2 differentially activated by ADP-ribose an  
 RT hydrogen peroxide.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20285799; PubMed=10830953;  
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,  
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,  
 RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,  
 RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,  
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,  
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,  
 RA Shintani A., Sasaki T., Nagamine K., Mitsuoyama S., Antonarakis S.E.,  
 RA Minoshima S., Shimizu N., Nordliek G., Hornischer K., Brandt P.,  
 RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,  
 RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,  
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

RA Lehrach H., Reinhardt R., Yaspo M.-L.;  
 RT "The DNA sequence of human chromosome 21.";  
 RL Nature 405:311-319(2000).  
 CC -!- FUNCTION: MAY BE A CALCIUM CHANNEL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -!- ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (shown here) and 2;  
 CC are produced by alternative splicing.  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. LTRPC  
 CC SUBFAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AB001535; BAA34700.1; -;  
 CC EMBL; AJ417076; CAD01139.1; -;  
 CC EMBL; AP001754; BAA95563.1; -;  
 CC Genew; HGNC:12339; TRPM2.  
 CC MIN; 603749; -;  
 CC InterPro; IPR002111; Cat\_channel\_TrpL.  
 CC InterPro; IPR000636; M\_channel\_nlg.  
 CC InterPro; IPR002153; Trans\_recep.  
 CC Pfam; PF00520; Ion\_trans; 1.  
 CC PRINTS; PR01097; TRNSRECEPT.  
 CC DR Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 KW Alternative splicing.  
 FT DOMAIN 1 752 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 753 773 POTENTIAL.  
 FT DOMAIN 774 795 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 796 816 POTENTIAL.  
 FT DOMAIN 817 820 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 821 841 POTENTIAL.  
 FT DOMAIN 842 896 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 897 917 POTENTIAL.  
 FT DOMAIN 918 936 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 937 957 POTENTIAL.  
 FT DOMAIN 958 1025 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1026 1046 POTENTIAL.  
 FT DOMAIN 1047 1503 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1504 1503 POTENTIAL.  
 FT VARSPLIC 538 557 MISSING (IN ISOFORM 2).  
 FT VARSPLIC 1291 1325 DTLEPLSTIQYNVVDGLRDRSRFHGYPYVOAGLPL -> E  
 FT CONFLICT 1088 1088 S -> N (IN REF. 2).  
 FT CONFLICT 1189 1189 R -> Q (IN REF. 3).  
 FT SEQUENCE 1503 AA; 171225 MW; AD329AE79F1A71B5 CRC64;  
 Query Match 3.4%; Score 155; DB 1; Length 1503;  
 Best Local Similarity 22.4%; Pred. No. 0.035;  
 Matches 72; Conservative 46; Mismatches 98; Indels 106; Gaps 11;  
 QY 469 VSFYINVSVYLCAMVITLTAYYQPLEGTPPYPTVDVLR-----AGEVITLF-----519  
 Db 797 VVFLNLTSLYFAFLCLF---AYLVMDVFQVPVSCCAIYLVLSFVCEEMRQLFYDPDE 853  
 QY 520 -----TGVLFEEFTNIKDLFMKCPGVNSLFTDGSFQLLYFIYSVLVIVSAALYAGIEAY 574  
 Db 854 CGLMKKAALYF---SDFWNKLDVGAILLFVAG-----LTCRLIPATLYPGRVILS 900  
 QY 575 LAVNVFALVIGWMNALYFTTGLKLTGYYSIMIOIKFLKDFRFLVLLFMIGYASALVS 634  
 Db 901 LDFILFCLRLMHIFTISKTLGPK-----IIIVKRMKMDVFFFLFLAVVWVSVGAKQA 954  
 QY 635 LL-----NPKANKVNCVEDQTNCTVPTPS 659  
 Db 955 ILIHNERRVDWLFPRGAYVHSYLTIFGQIPGYIDGVNFPN-----EHCSS---PNETDPYKPK 1007  
 QY 660 CRSEFTSTFLDLFKLTICMGDLEMSLSTKYPVVF-----IILLVYIILTFLVLLNML 714

Pfam:	PF00520;	ion_trans; 1
DR	PRINTS:	PROI097; TRNSRECEPTP.
DR	TIGRFAMS:	TIGR00870; trp; 1.
DR	PSOITE:	PS50088; ANK_REPEAT; FALSE NEG.
DR	PROSITE:	PS0297; ANK_REPEAT_REGION; FALSE NEG.
KW	Ionic channel:	Transmembrane; Ion transport; Calcium channel;
KW	ANK repeat:	Repeat; Glycoprotein.
FT	DOMAIN	1 369 CYTOPLASMIC (POTENTIAL).
FT	TRANSEM	370 390 POTENTIAL.
FT	DOMAIN	391 418 EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	419 439 POTENTIAL.
FT	DOMAIN	440 451 CYTOPLASMIC (POTENTIAL).
FT	TRANSEM	452 472 POTENTIAL.
FT	DOMAIN	473 523 EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	524 544 POTENTIAL.
FT	DOMAIN	545 567 CYTOPLASMIC (POTENTIAL).
FT	TRANSEM	568 588 POTENTIAL.
FT	DOMAIN	589 637 EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	638 658 POTENTIAL.
FT	DOMAIN	659 836 CYTOPLASMIC (POTENTIAL).
FT	REPEAT	26 55 ANK 1.
FT	REPEAT	61 90 ANK 2.
FT	REPEAT	92 118 ANK 3.
FT	REPEAT	147 176 ANK 4.
FT	CARBOHYD	404 404 N-LINKED (GLCNAC... ) (POTENTIA
SQ	SEQUENCE	836 AA; 95671 MW; 7B863B209B9A25F8 CRC64;
Query Match		
Best Local Similarity		
Matches 138; Conservative 102; Mismatches 221; Indels 238		
QY	210	IPVLDDTAERTGNMREFINSPFRDIYYRGQTALHAIERRCKHVVELL----
DB	40	IPVVKMLEESRTLN-VNC-----VDYMQNQLQAVGNEHLEVTLLKKKE
QY	258	----VAQG-----ADVHAQAQRFFOPKDGGGVFY
DB	94	LILAISKGYVRIVEAILGHPPGAASRRRLTLPCEQEELRDDDFAYDEGDGRTF
QY	291	LAACCTNOPHIYNYL-----TENPHKK-----ADMRROD--SRGNTVLHA
DB	154	LAAUCHKEYEVHLLLKGARIERAHDYFCRCSDCAEKORLDATFSHSRSRNA
QY	334	-----NTRENTREVTKM-----YDLLLKLC-----ARLF
DB	214	YLSLSEDPVLTALSNELAKLANIEKFKNRYKLMSMOCKDFVVGVDLDC
QY	365	VLNND--GLSLPMMAKTGKIQHIIIRREVTDTRHLRSFKFDWAYGPV
DB	274	ILNGDLSEAEPLEHRHGHKASLSRVLAIKYE-----KKFV--AHFNPCI
QY	422	-SSLDTCGEASVLEILVVYSNKIENRHMLAV-----EPIN
DB	323	YENUSGREQTIAKCLV-----VLVVALGPLFLAIGVIAPCSRIG
QY	465	KF--GAVSYFINWSYLCAWIFTLAYIQPLEGTPPYVRTTVDYLRUARGE
DB	373	KFYAHAASFII-----FLGLIVENSADR-EGITTLPTNIIVIDYPKPQIFR
QY	522	V-LFFTNIKDLFMKCCPGVNSLFIGDSFOLLYFIYSVL-----VIUSA-
DB	425	TEMLIMVMVLGMWMSEC---KELNWLEGPREYIVQLWNVLDFGMLSIFIAPT
QY	573	Ayla-----VMVFA
DB	482	ATRAAQYVDHSVQESDLSEVTLPEPVQYFYTYARDKWLPSPDQIISEGLYAIA
QY	590	LYFTFRGLKLTGTYSIMIKILFKDLFR-----FLLVYLLFMIG----YASALV
DB	542	AYILPANESFGPLQISLGRTV-KDIFKMVLFWIWFVLAFMIGHMFIILSYLIG
QY	642	MKVCSNETQNTCTPTYPEPCROSETSTFTSLDDLDFKLTIIGMGDMLEMLST-KYP













Qy	271	-----RFPQKDEGGYFVGELPUSLAACNQPHVNYL-----TENPHKK-----A	312
		: :       :       :       :       :	
Db	141	ELQDDDFAYDEDGTRESPTTPIIAAHQCQKVVEVHMLLMKGARTERHDVFCCKGDCM	200
		: :       :       :       :       :	
Qy	313	DMRRODSRGNT-----VLHAL-----VAIADNTRENTX-----	340
		: :       :       :       :       :	
Db	201	EQRHDSFSHSRINAYKGLASPAYSLSSEDPVLTALSLELNELAKLANIEKFENDXR	260
		: :       :       :       :       :	
Qy	341	-----FVTKMYYDLLLLKCARLPDPSNLEAVLNND--GLSPILMAAAKTGKIGIFQHII	390
		: :       :       :       :       :	
Db	261	KLSMOCKDFVGVGLDL-----CR--DSEEVEAILNGDLESAPLEPVHRHKASLSRVKLAI	313
		: :       :       :       :       :	
Qy	391	REVTVDETRHLRSRKFKDWAGPYVSSISYDL--SSLDTCGEASVLEILLVYNYSKIENRHE	448
		: :       :       :       :       :	
Db	314	KTEV-----KKFV--AHPNCQQQLLIWTWENSGLREQTLIAKCLV-----	352
		: :       :       :       :       :	
Qy	449	MNAV-----EPINELLDRKWRKF--GAVSFYINVVSYLCAVMVIFTLAY	490
		: :       :       :       :       :	
Db	353	VLVVALGPLFLAIGYWIAPSRLGKILURSPFMFVAHAASFJ-----FLGLVFNASDR	407
		: :       :       :       :       :	

QY	491	YQPLEGTPPYR	TTVDYLR	LAGEV-ITL	TGV-LFF	FTN	KDLFM	KKCP	GVNSL	FIDGS	548
		:			:		:	:	:		:
Db	408	F---	EGIT	TLENIT	VDYD	PKOIF	RKTKT	QTTW	EMLIM	VWVLGM	461
		:	:	:	:	:	:	:	:	:	:
QY	549	FOLLY	FXISV	L-----	VIVSA--	ALY	LAGEA	YLA-----			576
		:	:	:	:	:	:	:	:	:	:
Db	462	REY	ILQ	MNV	LDF	CGML	SIF	NAFT	ARFLA	LOATK	400
		:	:	:	:	:	:	:	:	:	:
QY	577	-----	-----	-----	VNV	FAL	VIG	MN	ALY	FTRG	KL
		:	:	:	:	:	:	:	:	:	:
Db	522	FTY	ARD	KWLP	SDP	QI	ISE	GLYA	IAV	AFS	RIAY
		:	:	:	:	:	:	:	:	:	:
QY	618	LLV	LLFM	IG	YAS	AL	VS	LLN	PC	NKVC	NED
		:	:	:	:	:	:	:	:	:	:
Db	581	MVL	FTM	FWF	FMI	GM	FIL	YSY	LGA	KV-----	NA
		:	:	:	:	:	:	:	:	:	:
QY	678	IGM	GLE	MLS	ST-KYP	VVVF	-----	ILL	VTY	YI	LT
		:	:	:	:	:	:	:	:	:	:
Db	630	-----	EY	SV	LV	KYD	HK	F	EN	IGY	V
		:	:	:	:	:	:	:	:	:	:
QY	732	IWK	734								
		:	:								
Db	684	EWK	686								
		:	:								

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Query Match          3.2%; Score 148; DB 1; Length 848;
Best Local Similarity 19.1%; Pred. No. 0.046;
Matches 138; Conservative 104; Mismatches 243; Indels 238; Gaps 33;
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OY 185 FREPSTGKTCLPKALLNLNSGRNDTIPVLDDTAERTGNWREFINSFRIYVRGPOTALHI 244  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 29 FNDRGTSLTAESEERFLDAAEYGN--IPVVKMLLEESKTLN--VNC-----VDVMGONALQL 80

OY 245 ATERCKKHVVLLVAQ-----GADVHAQAQG-----270  
| : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 81 AVGNEHLEYTEULLKKENIARIGCDALLAISGYRIVEAIIINHPGFSAKRUTLSPCEQ 140

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2003, 19:49:48 ; Search time 72 Seconds  
(without alignments)

1610.112 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSEGPACGEVAELPG.....PRCDGHQGYPRKWRDAP 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	4577	100.0	871	22	AAG65787		Human ion channel
2	4577	100.0	871	22	AAE01227		Human vanilloid re
3	4577	100.0	871	23	ABB79191		Human VR4 protein
4	4577	100.0	871	23	AAU74935		Amino acid sequenc
5	4571	99.9	871	22	AAE06681		Human vanilloid re
6	4558	99.6	963	21	AAV96479		Human vanilloid re
7	4558	99.6	963	23	AAU95381		Human calcium tran
8	4546	99.3	871	22	AAG67210		Amino acid sequenc
9	4387	95.8	871	22	AAB86980		Murine OTRPC4 prot
10	4374	95.6	871	22	AAG67209		Amino acid sequenc

11	4218	92.2	811	22	AAE06682		Human vanilloid re
12	4215	92.1	803	22	AAG63208		Amino acid sequenc
13	3868	84.5	743	22	AAG63209		Amino acid sequenc
14	3829	83.7	742	22	AAE06683		Human vanilloid re
15	3121.5	68.2	602	23	AAO74936		Amino acid sequenc
16	2898.5	63.3	559	23	AAE16773		Human transporter
17	2547	55.6	498	22	AAE04889		Novel human diagno
18	2315.5	50.6	1115	22	ABG28242		Chicken capsaicin
19	1845.5	40.3	843	20	AAV06561		Human vanilloid re
20	1842.5	40.3	843	20	AAW99799		Human capsaicin re
21	1818	39.7	838	20	AAV06555		Rat capsaicin rece
22	1818	39.7	838	20	AAW99789		Rat VR1 capsaicin
23	1818	39.7	838	22	AAE01228		Rattus vanilloid r
24	1801	39.3	839	21	AAV97357		Human VR-1 protein
25	1801	39.3	839	22	AAE01229		Human vanilloid re
26	1800	39.3	839	20	AAV30155		A human vanilloid
27	1800	39.3	839	20	AAV06558		Human capsaicin re
28	1800	39.3	839	21	AAV30152		Human vanilloid re
29	1796	39.2	839	20	AAV30152		A human vanilloid
30	1796	39.2	839	20	AAV30153		Human vanilloid re
31	1795	39.2	839	21	AAV96478		Human vanilloid re
32	1497.5	32.7	761	20	AAV06556		Rat vanilloid rece
33	1497.5	32.7	761	20	AAW99790		Rat VRP-1 (VR2) c
34	1472.5	32.2	763	20	AAV42308		Human vanilloid re
35	1472.5	32.2	763	20	AAV29471		Human vanilloid re
36	1468	32.1	764	22	AAE04890		Human transporter
37	1467	32.1	764	20	AAV29469		Human vanilloid re
38	1467	32.1	764	20	AAV06559		Human vanilloid re
39	1467	32.1	764	21	AAV97358		Human VR-2 protein
40	1467	32.1	764	22	AAV35622		Human vanilloid re
41	1467	32.1	764	23	ABB07817		Human vanilloid re
42	1467	32.1	764	23	AAV51859		Human vanilloid re
43	1464	32.0	764	22	AAE01230		Human vanilloid re
44	1456.5	31.8	764	21	AAV84834		Amino acid sequenc
45	1454.5	31.8	764	23	ABB07818		Human vanilloid re

#### ALIGNMENTS

RESULT 1  
AAG65787  
ID AAG65787 standard; Protein; 871 AA.  
XX  
AC AAG65787;  
XX  
DT 30-JAN-2002 (first entry)  
XX Human ion channel VR-5 protein sequence.  
DE  
XX  
XX Ion channel; vanilloid receptor; VR-3; VR-5; nootropic; neuroprotective;  
KW antiparkinsonian; analgesic; antidiabetic; antiproliferative; cytostatic;  
KW antirheumatic; antiarthritic; gene therapy; antisense therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200168857-A2,  
XX  
PD 20-SEP-2001.  
XX  
PF 15-MAR-2001; 2001WO-US08329.  
XX  
PR 15-MAR-2000; 2000US-0525420.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Curtis RAJ, Cook WJ;  
XX  
DR WPI; 2001-596911/67.  
DR N-PSDB; AAI66972, AAI66973.  
XX  
PT Nucleic acid encoding human ion channels referred to as Vanilloid  
receptor 3 (VR-3) and VR-5, useful for screening modulators of VR-3 or

PT VR-5 and for treating calcium homeostasis related disorders (e.g. dementia) and pain disorders -

PS Claim 13; Fig 2A-C; 167pp; English.

CC The invention provides nucleic acid encoding human ion channels referred to as vanilloid receptor 3 (VR-3) and VR-5. The VR-3 or VR-5 proteins can be used to screen for naturally occurring VR-3 or VR-5 ligands or for drugs or compound which modulate VR-3 or VR-5 activity. The VR-3 or VR-5 proteins and their modulators (e.g. antisense nucleic acids and anti-VR antibodies) are useful for treating disorders characterized by insufficient or excessive production of VR-3 or VR-5. These disorders are calcium homeostasis related disorders (Alzheimer's disease, dementia, Parkinson's disease), pain disorders (diabetic neuropathy, rheumatoid arthritis) and/or cellular growth and/or proliferation disorders (e.g. cancer). Numerous other examples of these disorders are given in the specification. The present sequence represents the human VR-5.

XX Sequence 871 AA;

SQ

Query Match 100.0%; Score 4577; DB 22; Length 871;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPACGGEVAELPGDESGTPGCEAPPLSSLANLFEGEDGSLSPADASRPAGP 60

DB 1 MADSEGPACGGEVAELPGDESGTPGCEAPPLSSLANLFEGEDGSLSPADASRPAGP 60

QY 61 GDGRPNLRMKFGQAFRGVNPIDLLSTLVSSVPGPKAPMDSLFDYGYRHHSSDN 120

DB 61 GDGRPNLRMKFGQAFRGVNPIDLLSTLVSSVPGPKAPMDSLFDYGYRHHSSDN 120

QY 121 KRRKKIIEKQSPQSPKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLLFLTHKKRL 180

DB 121 KRRKKIIEKQSPQSPKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLLFLTHKKRL 180

QY 181 TDEFRPSTGKTLCPKALLNSGRNDTIPVLIDIAERTGNMREFINSPPRDIIYRGQT 240

DB 181 TDEFRPSTGKTLCPKALLNSGRNDTIPVLIDIAERTGNMREFINSPPRDIIYRGQT 240

QY 241 ALHTAIRRCKHYVELLYVAQADYHAQARGFFQKDEGGYFEGELPLSLAAGTNPQHI 300

DB 241 ALHTAIRRCKHYVELLYVAQADYHAQARGFFQKDEGGYFEGELPLSLAAGTNPQHI 300

QY 301 VNYLTENPHKKADMRRODSRGNTVHLVAIADNTRENTKFTVMYDILLKLCARLPDPS 360

DB 301 VNYLTENPHKKADMRRODSRGNTVHLVAIADNTRENTKFTVMYDILLKLCARLPDPS 360

QY 361 NLEAVLNNDGSLPLMMAAKTKIGIFQHIIRREVTDEDTLHLSRKFQDWAYGPVYSSLYD 420

DB 361 NLEAVLNNDGSLPLMMAAKTKIGIFQHIIRREVTDEDTLHLSRKFQDWAYGPVYSSLYD 420

QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINWVSYL 480

DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINWVSYL 480

QY 481 AMWIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 540

DB 481 AMWIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 540

QY 541 NSLFDGSQLLYFIYSVLTVSAALYLAGIEALVAVFALVGLGWNALYFTRLGLKTG 600

DB 541 NSLFDGSQLLYFIYSVLTVSAALYLAGIEALVAVFALVGLGWNALYFTRLGLKTG 600

QY 601 TYSIMQIKILFKDLFRELLVYLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVPTPSC 660

DB 601 TYSIMQIKILFKDLFRELLVYLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVPTPSC 660

QY 661 RDSFTFTFLDLFLKLTIGMDLMLSTKYPVVFIIILVYIILTVLLNMLIALMGE 720

DB 661 RDSFTFTFLDLFLKLTIGMDLMLSTKYPVVFIIILVYIILTVLLNMLIALMGE 720

QY 721 TVGQVSKESKHWKQWATLTIERSFPVFLRKAFRSGEMVTYVKSSDGTDPDRWCFRV 780

DB 721 TVGQVSKESKHWKQWATLTIERSFPVFLRKAFRSGEMVTYVKSSDGTDPDRWCFRV 780

QY 781 DEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTYGRLLRRDRWSSVYPRVVELNKNSPDE 840

DB 781 DEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTYGRLLRRDRWSSVYPRVVELNKNSPDE 840

QY 841 VVPLDSMGNPRCDGHOOGYPRKWRRTDAP 870

DB 841 VVPLDSMGNPRCDGHOOGYPRKWRRTDAP 870

RESULT 2

AAE01227

ID AAE01227 standard; Protein; 871 AA.

XX AAE01227;

XX 31-JUL-2001 (first entry)

XX Human vanilloid receptor 3 (hVR3) protein.

XX Human: vanilloid receptor 3; VR3; inflammation; arthritis; psoriasis;

XX wound healing; analgesic; vulnery; antiallergic; gene therapy;

XX neuropathic pain; rhinitis; pruritus; bladder dysfunction;

XX cluster headache; capsaicin-sensitive ion channel disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 238..269

XX Domain /label= Ankaryn\_repeat

XX Domain 284..316

XX Domain /label= Ankaryn\_repeat

XX Domain 369..402

XX Domain /label= Ankaryn\_repeat

XX Domain 470..491

XX Domain /label= Transmembrane\_domain

XX Domain 515..535

XX Domain /label= Transmembrane\_domain

XX Domain 551..570

XX Domain /label= Transmembrane\_domain

XX Domain 575..593

XX Domain /label= Transmembrane\_domain

XX Domain 617..635

XX Domain /label= Transmembrane\_domain

XX Region 667..681

XX Domain /label= Poor\_loop\_region

XX Domain 693..720

XX Domain /label= Transmembrane\_domain

XX WO200134805-A2.

XX 17-MAY-2001.

XX 10-NOV-2000; 2000WO-US31077.

XX 12-NOV-1999; 99US-0438997.

XX (ABBO ) ABBOTT LAB.

XX Masters JN, Vos MH;

XX WPI; 2001-335930/35.

XX N-PSDB; AAD05107.

XX Novel human vanilloid receptor gene and encoded polypeptides for

XX identifying compounds that modulate vanilloid receptors in human

XX tissues and for treating inflammation, arthritis, psoriasis and wound

XX healing

XX Claim 18; Fig 8; 91pp; English.



CC The present sequence is human vanilloid receptor 3 (hVR3) protein.  
CC Vanilloid receptor protein and its DNA are useful for identifying  
CC compounds which modulate vanilloid receptors in human tissues, which are  
CC useful for treating various disease states, including neuropathic pain,  
CC inflammation, arthritis, rhinitis, pruritus, bladder dysfunction, cluster  
CC headache, wound healing and psoriasis. Vanilloid receptor DNA is useful  
CC as standard or reagent in diagnostic immunoassays, as targets for  
CC pharmaceutical screening assays and also in gene therapy. Vanilloid  
CC receptor protein is useful for detecting the presence of anti-vanilloid  
CC receptor derived polypeptide in test samples. Vanilloid receptor  
CC antibodies are useful for detecting vanilloid receptor polypeptides, for  
CC screening for diseases or conditions associated with abnormal vanilloid  
CC receptor production, treating disorders involving capsacin-sensitive  
CC ion channels and as diagnostic markers.  
XX  
SQ

Sequence 871 AA;  
Query Match 100.0%; Score 4577; DB 22; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADSSGPRAGCEVAELPDESGTGGEGAPFLSSLANLFEEDGSLSPADASRPPAG 60  
DB 1 MADSSGPRAGCEVAELPDESGTGGEGAPFLSSLANLFEEDGSLSPADASRPPAG 60  
QY 61 GDGRPNLRMKFOGAFKRGVNPIDLLLESTLYESSVPGPKKAPMDSLFYGYTRHSSDN 120  
DB 61 GDGRPNLRMKFOGAFKRGVNPIDLLLESTLYESSVPGPKKAPMDSLFYGYTRHSSDN 120  
QY 121 KRRKKIIEKQSPKAPAPQPPPIKLVFNRPIDFIVSRGSTADLDGLLPLFLTHKKRL 180  
DB 121 KRRKKIIEKQSPKAPAPQPPPIKLVFNRPIDFIVSRGSTADLDGLLPLFLTHKKRL 180  
QY 181 TDEEFREPSTGKTLCPKALLNLSNGRNDTIPVLLDJAERTGNMREFINSPFRDIYRGOT 240  
DB 181 TDEEFREPSTGKTLCPKALLNLSNGRNDTIPVLLDJAERTGNMREFINSPFRDIYRGOT 240  
QY 241 ALHAIERRCKHYVELLVAGQADVHAQAARGRFQPKDEGGYFYFEGELPLSLAACTNPHI 300  
DB 241 ALHAIERRCKHYVELLVAGQADVHAQAARGRFQPKDEGGYFYFEGELPLSLAACTNPHI 300  
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKVFYTKMYDLLLLKCARLPDS 360  
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKVFYTKMYDLLLLKCARLPDS 360  
QY 361 NLEAVLNNDGLSLPMAAATGKIGIFQHIIRREVTEDTRHLSRKFKDWAYGVPVSSLYD 420  
DB 361 NLEAVLNNDGLSLPMAAATGKIGIFQHIIRREVTEDTRHLSRKFKDWAYGVPVSSLYD 420  
QY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLEC 480  
DB 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLEC 480  
QY 481 AMVIFLTAYQPLEGTPPYPTTVDYLRAGEVITLFTGVLFFFNTNKDLPMKKCPGV 540  
DB 481 AMVIFLTAYQPLEGTPPYPTTVDYLRAGEVITLFTGVLFFFNTNKDLPMKKCPGV 540  
QY 541 NSLFDIGSFOLLYFIYSVLVISAALYLAGIEAYLAVMVFALVGLGMNALLYFRGLKLTG 600  
DB 541 NSLFDIGSFOLLYFIYSVLVISAALYLAGIEAYLAVMVFALVGLGMNALLYFRGLKLTG 600  
QY 601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALYSLNPNCKMKNVCNEDQTNCTVPTPSC 660  
DB 601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALYSLNPNCKMKNVCNEDQTNCTVPTPSC 660  
QY 661 RDSSETSTFLDLFKLTIGMDLEMLSSSTKYPVFFIILVYIILFVLLNMLIALMGE 720  
DB 661 RDSSETSTFLDLFKLTIGMDLEMLSSSTKYPVFFIILVYIILFVLLNMLIALMGE 720  
QY 721 TVGQVSKESKHINKLOWATTILDIERSEFPVFLKAFRSGEMVTGKSSDGTDPDRRCFRV 780  
DB 721 TVGQVSKESKHINKLOWATTILDIERSEFPVFLKAFRSGEMVTGKSSDGTDPDRRCFRV 780

QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRULRRDRWSSVVRVVELNKNNSPDE 840  
DB 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRULRRDRWSSVVRVVELNKNNSPDE 840  
QY 841 VVPLDSMGNPRCDGHOOGYPRKWRTPDAP 870  
DB 841 VVPLDSMGNPRCDGHOOGYPRKWRTPDAP 870  
RESULT 3  
ABB79191  
ID ABB79191 standard; Protein; 871 AA.  
XX AC ABB79191;  
XX DT 07-AUG-2002 (first entry)  
XX DE Human VR4 protein SEQ ID NO:2.  
XX KW Human; VR4; vanilloid 4 receptor; receptor; osteopathic; antirheumatic;  
XX KW antirheumatic; vulnery; analgesic; gene therapy; cartilage; bone;  
XX KW larynx; auditory canal; intravertebral disc; ligament; tendon;  
XX KW joint capsule; bone development disorder; osteoporosis; osteoarthritis;  
XX KW joint destruction; rheumatoid arthritis.  
XX OS Homo sapiens.  
XX PN WO200234280-A2.  
XX PD 02-MAY-2002.  
XX PF 25-OCT-2001; 2001WO-GB04739.  
XX PR 25-OCT-2000; 2000GB-0026114.  
XX PA (SMIK ) SMITHLINE BEECHAM PLC.  
XX PI Davis JB, Gunthorpe MJ, Egerton J, Smart D;  
XX WPI: 2002-471426/50.  
XX N-PSDB; ABN87645.  
XX Use of vanilloid 4 receptor polypeptide/polynucleotide, a modulator of  
XX the polypeptide or an antisense polynucleotide to the polynucleotide,  
XX for manufacture of a medicament for treating cartilage and/or bone  
XX diseases  
XX Claim 8; Page 22; 30pp; English.  
XX The present sequence represents human vanilloid 4 receptor (VR4). VR4  
XX has osteopathic, antirheumatic, antiarthritic, vulnery and analgesic  
XX activities. VR4 proteins and polynucleotide sequences can be used in  
XX modulating VR4 activity, in gene therapy and in antisense gene therapy.  
XX VR4 is useful for the manufacture of a medicament for treating diseases  
XX of cartilage and/or bone, or for the treatment of pain associated with  
XX it, where the disease is one affecting the larynx, auditory canal,  
XX intravertebral discs, ligaments, tendons and joint capsules, or a  
XX disease associated with bone development including osteoporosis, or  
XX diseases involving joint destruction such as rheumatoid arthritis or  
XX osteoarthritis, and the pain is associated with rheumatoid arthritis  
XX or osteoarthritis.  
XX Sequence 871 AA;  
Query Match 100.0%; Score 4577; DB 23; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADSSGPRAGCEVAELPDESGTGGEGAPFLSSLANLFEEDGSLSPADASRPPAG 60  
DB 1 MADSSGPRAGCEVAELPDESGTGGEGAPFLSSLANLFEEDGSLSPADASRPPAG 60  
QY 61 GDGRPNLRMKFOGAFKRGVNPIDLLLESTLYESSVPGPKKAPMDSLFYGYTRHSSDN 120

Db 61 GGRPNLRMKFGAQRKGVNPDIDLESTLYESSVPGPKAPMDSLFDYGYRHHSSDN 120  
QY 121 KWRKKIIEKQPSQSPKAPAPPPILKVFNRPIEDIVSRGSTADLGLPPLLTHKKRL 180  
Db 121 KWRKKIIEKQPSQSPKAPAPPPILKVFNRPIEDIVSRGSTADLGLPPLLTHKKRL 180  
QY 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGQT 240  
Db 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGQT 240  
QY 241 ALHIAIERCKHYVELLVAGQADVHAQAGRFQPKDEGGYFYFGELPLSLAACTNQHPI 300  
Db 241 ALHIAIERCKHYVELLVAGQADVHAQAGRFQPKDEGGYFYFGELPLSLAACTNQHPI 300  
QY 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLPDPS 360  
Db 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLPDPS 360  
QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFCDWAYGPVSSLYD 420  
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFCDWAYGPVSSLYD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFVNVSYLC 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFVNVSYLC 480  
QY 481 AWIIFTLAYOPLGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540  
Db 481 AWIIFTLAYOPLGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540  
QY 541 NSLFDGSGFOLLFYFYSVLVIVSAALYLAGIEAVLAVMVFALVGLGWMNALYFTRGLKLTG 600  
Db 541 NSLFDGSGFOLLFYFYSVLVIVSAALYLAGIEAVLAVMVFALVGLGWMNALYFTRGLKLTG 600  
QY 601 TYSIMQIKLFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660  
Db 601 TYSIMQIKLFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660  
QY 661 RDETFSTFLDLKLTGMDGLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720  
Db 661 RDETFSTFLDLKLTGMDGLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720  
QY 721 TVGOVSKESKHIWKLQWATTILDIERSPFVLRKAFRSGEMVTGKSSDGTDDRWCFRV 780  
Db 721 TVGOVSKESKHIWKLQWATTILDIERSPFVLRKAFRSGEMVTGKSSDGTDDRWCFRV 780  
QY 781 DEVNMSHNQNLGIINEDPGKNETYQYGFSTYGRRLRRDRWSSVPRVVELNKNPNDE 840  
Db 781 DEVNMSHNQNLGIINEDPGKNETYQYGFSTYGRRLRRDRWSSVPRVVELNKNPNDE 840  
QY 841 VVPLDSMGNPRCDGHOOGYPRKWRDTDDAP 870  
Db 841 VVPLDSMGNPRCDGHOOGYPRKWRDTDDAP 870

RESULT 4  
AAU74935  
ID AAU74935 standard; Protein: 871 AA.  
XX AC AAU74935;  
XX AC AAU74935;  
XX DT 23-APR-2002 (first entry)  
XX DE Amino acid sequence of human vanilloid receptor-like protein 2a (VRL-2a).  
XX KW Human; vanilloid receptor-like protein 2a; VRL-2a; hypertension;  
KW ion-channel protein; pain; osteoarthritis; diabetic neuropathy;  
KW neuralgia; nerve injury; neurodegeneration; stroke; inflammation;  
KW asthma; allergy; urogenital disorder; incontinence; hypotension;  
KW perivascular disease; VRL-related disease; receptor.  
XX OS Homo sapiens.

XX PN EP1160254-AL.  
XX PD 05-DEC-2001.  
XX PF 25-MAY-2001; 2001EP-0304663.  
XX PR 31-MAY-2000; 2000US-208156P.  
XX PA (PFIZ ) PFIZER INC.  
XX PI Shinjo K, Yabuuchi H;  
XX DR WPI: 2002-084359/12.  
XX PT N-PSDB; ABK14002.  
XX PS New human vanilloid receptor-like proteins, useful for identifying modulators for e.g. treating pain, also related nucleic acid  
XX Claim 1: Page 17-18; 32pp; English.  
XX The present invention relates to a new polypeptide that has a sequence  
XX 871 amino acids (AAU74935) or 602 amino acids (AAU74936) long, or their  
XX variants, as defined in the specification. The polypeptide of the  
XX invention is deduced from a human nucleic acid 2749 base pairs (ABK14002)  
XX or 1900 base pairs (ABK14003) long, or their variants, also defined in  
XX the specification. The polypeptides of the invention, which are human  
XX vanilloid receptor-like (VRL) proteins, are used to identify specific  
XX modulators that are potentially useful for treating pain (of any origin),  
XX osteoarthritis, (diabetic) neuropathy, neuralgia, nerve injury,  
XX neurodegeneration, stroke, inflammation, asthma, allergy, urogenital  
XX disorders, incontinence, hypo- or hyper-tension and perivascular disease.  
XX The molecules of the invention can also be used to raise specific  
XX antibodies. The nucleic acid that encodes the polypeptide of the  
XX invention is useful for recombinant production of the protein and for  
XX preparing transgenic animal models. The polypeptide, antibody and for  
XX acid of the invention are also useful as diagnostic agents for  
XX determining (susceptibility to) VRL-related diseases. The present amino  
XX acid sequence represents the human vanilloid receptor-like protein 2a  
XX (VRL-2a) of the invention.  
XX Sequence 871 AA;

Query Match 100.0%; Score 4577; DB 23; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MADSEGPAGPGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRAGP 60  
Db 1 MADSEGPAGPGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRAGP 60  
Qy 61 GGRPNLRMKFGAQRKGVNPDIDLESTLYESSVPGPKAPMDSLFDYGYRHHSSDN 120  
Db 61 GGRPNLRMKFGAQRKGVNPDIDLESTLYESSVPGPKAPMDSLFDYGYRHHSSDN 120  
Qy 121 KWRKKIIEKQPSQSPKAPAPPPILKVFNRPIEDIVSRGSTADLGLPPLLTHKKRL 180  
Db 121 KWRKKIIEKQPSQSPKAPAPPPILKVFNRPIEDIVSRGSTADLGLPPLLTHKKRL 180  
Qy 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGQT 240  
Db 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGQT 240  
Qy 241 ALHIAIERCKHYVELLVAGQADVHAQAGRFQPKDEGGYFYFGELPLSLAACTNQHPI 300  
Db 241 ALHIAIERCKHYVELLVAGQADVHAQAGRFQPKDEGGYFYFGELPLSLAACTNQHPI 300  
Qy 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLPDPS 360  
Db 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLPDPS 360  
Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFCDWAYGPVSSLYD 420  
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFCDWAYGPVSSLYD 420

Db 361 NLEAVLNNDGLSPMLAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGVPYSSLYD 420  
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVVSYLK 480  
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVVSYLK 480  
 Qy 481 AMVIFTLAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 540  
 Db 481 AMVIFTLAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 540  
 Qy 541 NSLFDGSPOLLFIYISVLVISAALYAGIEAYLAVWVFALVGLWNALYFTFRLGLKLTG 600  
 Db 541 NSLFDGSPOLLFIYISVLVISAALYAGIEAYLAVWVFALVGLWNALYFTFRLGLKLTG 600  
 Qy 601 TYSIMIOKILFKDLFRLLVYLLPMIGYASALVSLNPNCKMVCNEDQNTCTVPTPSC 660  
 Db 601 TYSIMIOKILFKDLFRLLVYLLPMIGYASALVSLNPNCKMVCNEDQNTCTVPTPSC 660  
 Qy 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
 Db 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
 Qy 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
 Db 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
 Qy 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRLLRDRWSSVPRVVELNKNSPDE 840  
 Db 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRLLRDRWSSVPRVVELNKNSPDE 840  
 Qy 841 VVPLDSMGNPRCDGHOOQYPRKWRDTDDAP 870  
 Db 841 VVPLDSMGNPRCDGHOOQYPRKWRDTDDAP 870

## RESULT 5

AAE06681  
 ID AAE06681 standard; Protein; 871 AA.

AC AAE06681;

XX 16-OCT-2001 (first entry)

XX Human vanilloid receptor VR3 isoform, VR3A+B-.

XX Human: vanilloid receptor; VR3; inflammatory condition; analgesic;  
 KW intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;  
 KW postmastectomy pain; complex regional pain syndrome; arthritis;  
 KW rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;  
 KW chronic obstructive pulmonary disease; irritable bowel syndrome;  
 KW psoriasis; central nervous system disease; CNS; cancer;  
 KW intestinal tract disorder; VR3A+B-.

XX Homo sapiens.

OS W0200158945-A1.

XX 16-AUG-2001.

PF 01-FEB-2001; 2001WO-US03456.

XX 08-FEB-2000; 2000US-0500123.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Dublin AE, Huvar A, Glass CA, Erlander MG;

XX WPI: 2001-488969/53.

DR N-PSDB; AAD12791.

XX New human VR3 receptor useful for the treatment of disorders including  
 PT cancers arthritis and pain -  
 XX

PS Claim 11; Fig 3; 104pp; English.

CC The patent relates to human vanilloid receptor VR3 polynucleotide and  
 CC polypeptide. Three isoforms of VR3 namely VR3A+B-, VR3A-B- and VR3A+B-  
 CC have also been disclosed. The VR3 polypeptide is used to identify its  
 CC modulators which are useful for the treatment of inflammatory conditions  
 CC and for use as analgesics for intractable pain associated with  
 CC postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex  
 CC regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis),  
 CC as well as ulcers, neurodegenerative diseases, asthma, chronic  
 CC obstructive pulmonary disease, irritable bowel syndrome and psoriasis.  
 CC The VR3 modulators are also useful for treatment of central nervous  
 CC system (CNS) diseases, diseases of the intestinal tract, abnormal  
 CC proliferation and cancer. The present sequence is human VR3 receptor  
 CC isoform, VR3A+B-.

XX Sequence 871 AA;

Query Match 99.9%; Score 4571; DB 22; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 869; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPGEVAELPGDESGTSGEAPPLSSLANLFEDEGSLSPSPADASRAGP 60  
 Db 1 MADSSGPRAGPGEVAELPGDESGTSGEAPPLSSLANLFEDEGSLSPSPADASRAGP 60  
 Qy 61 GDGRPNURMKFQGAFRGVNPNIDLLSTLYESSVPPGPKAPMDSLFDGTGRHSSDN 120  
 Db 61 GDGRPNURMKFQGAFRGVNPNIDLLSTLYESSVPPGPKAPMDSLFDGTGRHSSDN 120  
 Qy 121 KRWKRIIEKQSPKAPAPQPPILKVFNRPLFDIVSRGSTADLGLLFLTHKKRL 180  
 Db 121 KRWKRIIEKQSPKAPAPQPPILKVFNRPLFDIVSRGSTADLGLLFLTHKKRL 180  
 Qy 181 TDEEFREPSTGKTCPLKALLNLSNGRNDTIPVLDIAERTGNMREFTNSFRDIYRGQT 240  
 Db 181 TDEEFREPSTGKTCPLKALLNLSNGRNDTIPVLDIAERTGNMREFTNSFRDIYRGQT 240  
 Qy 241 ALHTAIERRCKHYVELLVAOGADVHAQARGFPQKDEGGYFVFGELPLSLAAGTGNPHI 300  
 Db 241 ALHTAIERRCKHYVELLVAOGADVHAQARGFPQKDEGGYFVFGELPLSLAAGTGNPHI 300  
 Qy 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360  
 Db 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360  
 Qy 361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGVPYSSLYD 420  
 Db 361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGVPYSSLYD 420  
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVVSYLK 480  
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVVSYLK 480  
 Qy 481 AMVIFTLAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 540  
 Db 481 AMVIFTLAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 540  
 Qy 541 NSLFDGSPOLLFIYISVLVISAALYAGIEAYLAVWVFALVGLWNALYFTFRLGLKLTG 600  
 Db 541 NSLFDGSPOLLFIYISVLVISAALYAGIEAYLAVWVFALVGLWNALYFTFRLGLKLTG 600  
 Qy 601 TYSIMIOKILFKDLFRLLVYLLPMIGYASALVSLNPNCKMVCNEDQNTCTVPTPSC 660  
 Db 601 TYSIMIOKILFKDLFRLLVYLLPMIGYASALVSLNPNCKMVCNEDQNTCTVPTPSC 660  
 Qy 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
 Db 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
 Qy 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
 Db 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780

QY 781 DEVNHNQNLGIINEDPKNETYYGFSHTVGRRLRRDRSSVVRVVELNKNPNDE 840  
DB 781 DEVNHNQNLGIINEDPKNETYYGFSHTVGRRLRRDRSSVVRVVELNKNPNDE 840  
QY 841 VVPLDSMGNPCDGHQGGYPRKWRITDAP 870  
DB 841 VVPLDSMGNPCDGHQGGYPRKWRITDAP 870

RESULT 6  
AA96479  
ID AAY96479 standard; Protein; 963 AA.  
AC AAY96479;  
XX  
DT 12-SEP-2000 (first entry)  
DE Human vanilloid receptor 3.  
XX  
KW hVR3; vanilloid receptor; dorsal root ganglia; chromosome 12; capsaicin;  
KW marker D12S1893; nociceptor; calcium; influx; inhibitor;  
KW modulator; analgesic; uterine; anti-rheumatic; anti-arthritic;  
KW neuropathic; cerebroprotective; vasotropic; anti-asthmatic;  
KW anti-inflammatory; anti-migraine.

OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Binding-site 329..361  
FT /label= ankyrin\_binding\_domain  
FT Binding-site 376..408  
FT /label= ankyrin\_binding\_domain  
FT Binding-site 461..493  
FT /label= ankyrin\_binding\_domain  
FT Domain 561..583  
FT /label= transmembrane\_domain  
FT Domain 605..622  
FT /label= transmembrane\_domain  
FT Domain 638..660  
FT /label= transmembrane\_domain  
FT Domain 672..697  
FT /label= transmembrane\_domain  
FT Domain 707..725  
FT /label= transmembrane\_domain  
FT Domain 783..811  
FT /label= transmembrane\_domain

WO200032766-A1.  
08-JUN-2000.  
30-NOV-1999; 99WO-EP09284.  
01-DEC-1998; 98GB-0026359.  
(GLAXO) GLAXO GROUP LTD.  
Delany NS, Sanseau P, Tate SN;  
WPI: 2000-412315/35.  
N-PSDB; AAA29173.

Human vanilloid receptor protein or its variant useful for treating or preventing a disorder responsive to the modulation of hVR activity, such as pain, neuropathies, neuralgia, algesia, neurodegeneration.  
Claim 4; Fig 19; 135pp; English.  
Human VR1 is preferentially expressed in human dorsal root ganglia (DRG) and relative to hVR3 has the highest sequence homology with the rat VR1.  
The hVR3 gene maps to chromosome 17 near markers D12S177E and D12S1893.  
hVR1 is activated by capsaicin, the irritant in hot peppers. VRs are

CC nociceptors, transmitting nociceptive and thermoreceptive pain information  
CC back to pain-processing centres in the central nervous system. They are  
CC also sites for the release of pro-inflammatory mediators in the  
CC periphery. Capsaicin induces a flux of cations in DRG. The actions of  
CC capsaicin (excitation/desensitisation) are mediated by VRs. The natural  
CC ligand of the recently identified rat VR1 is unknown. It is possible that  
CC hVR sub-types may provide targets for the development of novel analgesic  
CC agents and agents which may interact with other disorders. hVR is useful  
CC for treatment or prophylaxis of a disorder responsive to the modulation  
CC of hVR activity, e.g. pain, neuropathic pain, inflammatory pain, chronic  
CC pain, post-operative pain, rheumatoid arthritis, stroke, ischaemia,  
CC neuralgia, algesia, neurodegeneration, nerve injury, respiratory disorder, asthma,  
CC migraine, irritable bowel syndrome (IBS), a respiratory disorder, asthma,  
CC chronic obstructive pulmonary disease (COPD), urological disorder,  
CC neuropathy, incontinence, interstitial cystitis or an inflammatory  
CC disorder in a human patient (claimed).

XX  
SQ Sequence 963 AA;

Query Match 99.6%; Score 4558; DB 21; Length 963;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 867; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPLSSLANLFEGEDGSLSPADASRPAGP 60  
DB 93 MADSEGPAGGGEVAELPGDESGTPGGEAPLSSLANLFEGEDGSLSPADASRPAGP 152  
QY 61 GDGRPNLRMKFGAFKGPVNPIDLESTLVESVVPKPKAPMDSLFDYGYRHHSSDN 120  
DB 153 GDGRPNLRMKFGAFKGPVNPIDLESTLVESVVPKPKAPMDSLFDYGYRHHSSDN 212  
QY 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIPLDIVSRGSTDADLGLLPLTHKKRL 180  
DB 213 KWRKKIIEKQPSKAPAPQPPILKVFNRPIPLDIVSRGSTDADLGLLPLTHKKRL 272  
QY 181 TDEFPREPSTCKTCLPKALLNLSGRNDTIPVLDDIAERTGNMREFINSPERDIYRGQT 240  
DB 273 TDEFPREPSTCKTCLPKALLNLSGRNDTIPVLDDIAERTGNMREFINSPERDIYRGQT 332  
QY 241 ALHAIERRCKHYVELLVAGQADVHAQARGFFPKDEGGYFYFGEPLSLAECTNPHI 300  
DB 333 ALHAIERRCKHYVELLVAGQADVHAQARGFFPKDEGGYFYFGEPLSLAECTNPHI 392  
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDPS 360  
DB 393 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDPS 452  
QY 361 NLEAVLNNDGLSPLMMAAKTKGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420  
DB 453 NLEAVLNNDGLSPLMMAAKTKGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 512  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSYFINVSYLC 480  
DB 513 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSYFINVSYLC 572  
QY 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLTGVLFFFTNKDLFKKCKPGV 540  
DB 573 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLTGVLFFFTNKDLFKKCKPGV 632  
QY 541 NSLFDGSGFOLLFYFYSVLVIVSAALYLAGIEAVLAVMVFALVGLWNNALYFTRGLKLTG 600  
DB 633 NSLFDGSGFOLLFYFYSVLVIVSAALYLAGIEAVLAVMVFALVGLWNNALYFTRGLKLTG 692  
QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 660  
DB 693 TYSIMIQILFKDLFRLLVYLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 752  
QY 661 RDSETFTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720  
DB 753 RDSETFTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 812  
QY 721 TVGVSKESKHVWKLOWATTITLIDERSPPVFLRAFRSGEMVTVGKSSDGTTPDRRCVFRV 780

Db 813 TVGOVSKESKHWKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCVRV 872  
Qy 781 DEVNWSHWNQNLGIINEDPKNETYQYGFSTHTVGRLLRRDRWSSVPRVVELNKNPNDE 840  
Db 873 DEVNWSHWNQNLGIINEDPKNETYQYGFSTHTVGRLLRRDRWSSVPRVVELNKNPNDE 932  
Qy 841 VVPLDSMGPRCDGHQOQYPRKWRDTDP 870  
Db 933 VVPLDSMGPRCDGHQOQYPRKWRDTDP 962

RESULT 7

AAU95381  
ID AAU95381 standard; Protein; 963 AA.

XX AAU95381;

DT 02-JUL-2002 (first entry)

XX Human calcium transport protein CatrF2E11.

XX Human; human leukocyte antigen; HLA; immunogen: 83P2H3; CatrF2E11;  
KW calcium transport protein; cancer; prostate cancer; cytostatic;  
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

OS W0200214361-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US25782.

XX 17-AUG-2000; 2000US-226329P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;  
PI Levin E, Hubert RS, Ge W, Jakobovits A;

XX WP1: 2002-269179/31.

XX N-PSDB; ABK67431.

PT Monitoring 83P2H3 gene products for monitoring the presence of cancer  
PT in a subject, comprises determining the status of 83P2H3 gene products  
PT in a tissue sample from the subject and comparing it to a normal sample

XX Example 1: Fig 2C-2D; 270pp; English.

XX The invention relates to monitoring 83P2H3 (a calcium transport  
CC protein whose gene is located on chromosome 7q34) gene products in a  
CC biological sample from a patient who has or is suspected of having  
CC cancer (especially prostate cancer), comprises: (a) determining the  
CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
CC an individual and (b) comparing the status to the status of 83P2H3 gene  
CC products in a normal sample. Also included are modulators of 83P2H3  
CC function or status, generating antibodies/immune response against  
CC 83P2H3 (or related protein CatrF2E11 whose gene is located on chromosome  
CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
CC peptides derived from the protein, delivering a cytotoxic agent to  
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
CC antibody, a recombinant protein comprising an antigen-binding region of  
CC the antibody, a non-human transgenic animal that produces the recombinant  
CC protein, a hybridoma that produces the recombinant protein, a single-  
CC chain monoclonal antibody that comprises the variable domains of the  
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
CC polynucleotide that encodes the monoclonal antibody and inducing an  
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
CC protein that comprises a T cell or B cell epitope, and contacting the  
CC epitope with an immune system T cell or B cell, respectively. The method  
CC is useful for monitoring 83P2H3 gene products in a biological sample for  
CC monitoring the presence of cancer in an individual. The modulator is

CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
CC treating cancer and the vector is useful for treating a patient with a  
CC cancer that expresses 83P2H3. The immunological methods are useful for  
CC generating an immune response against 83P2H3, and for detecting the  
CC presence of 83P2H3-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence  
CC is the protein sequence of 83P2H3 or its related protein CatrF2E11.

XX SQ Sequence 963 AA;

Query Match 99.68; Score 4558; DB 23; Length 963;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 867; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MADSEGPAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPPAG 60  
Db 93 MADSEGPAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPPAG 152  
Qy 61 GDGRPNLRMKFQGAFRKGVNPIIDLLLESTLYESSVPGPKAPMDSLFYGYTRHHSSDN 120  
Db 153 GDGRPNLRMKFQGAFRKGVNPIIDLLLESTLYESSVPGPKAPMDSLFYGYTRHHSSDN 212  
Qy 121 KWRKKIIEKQSPKAPAPPPPIILKVFNRPIILFIVSRGSGTADLDGLLFFLLTHKKRL 180  
Db 213 KWRKKIIEKQSPKAPAPPPPIILKVFNRPIILFIVSRGSGTADLDGLLFFLLTHKKRL 272  
Qy 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLDDIAERTGNMREINSPFRDIYRGOT 240  
Db 273 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLDDIAERTGNMREINSPFRDIYRGOT 332  
Qy 241 ALHAIATERCKHYVELLVAQADVHAQARGRFQPKDEBGYFYFEGELPLSLAACTNPHI 300  
Db 333 ALHAIATERCKHYVELLVAQADVHAQARGRFQPKDEBGYFYFEGELPLSLAACTNPHI 392  
Qy 301 VNYLTENPHKKADMRRODSRGNTVHLVAIAIADNTRENTKVFYTKMYDLLLLKCARLPDS 360  
Db 393 VNYLTENPHKKADMRRODSRGNTVHLVAIAIADNTRENTKVFYTKMYDLLLLKCARLPDS 452  
Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDDETRHLSRKFKDWAYGVPVSLYD 420  
Db 453 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDDETRHLSRKFKDWAYGVPVSLYD 512  
Qy 421 LSSLDTCGEEASVLEILVYNSKTENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLC 480  
Db 513 LSSLDTCGEEASVLEILVYNSKTENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLC 572  
Qy 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFFTNFKDLPKCPGV 540  
Db 573 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFFTNFKDLPKCPGV 632  
Qy 541 NSLFDGCSQQLLYFYISLVIVSAALYLAGIEAYLAMVYFALVGLGNMNAFYFRGLKLTG 600  
Db 633 NSLFDGCSQQLLYFYISLVIVSAALYLAGIEAYLAMVYFALVGLGNMNAFYFRGLKLTG 692  
Qy 601 TVYSIMIQILFKDLFRLLVYLFMTIGYASALVSLNPNCAKMKVCNEDQTNCTVTPYPS 660  
Db 693 TVYSIMIQILFKDLFRLLVYLFMTIGYASALVSLNPNCAKMKVCNEDQTNCTVTPYPS 752  
Qy 661 RSEFTSTFLLDLFKLTIGMDLEMSSTKYPVVFILLVTVIILTVILLVLLNMLIAMEG 720  
Db 753 RSEFTSTFLLDLFKLTIGMDLEMSSTKYPVVFILLVTVIILTVILLVLLNMLIAMEG 812  
Qy 721 TVGOVSKESKHWKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCVRV 780  
Db 813 TVGOVSKESKHWKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCVRV 872  
Qy 781 DEVNWSHWNQNLGIINEDPKNETYQYGFSTHTVGRLLRRDRWSSVPRVVELNKNPNDE 840

Db 873 DEVNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSNPDE 932

Qy 841 VVPLDSMGNPRCDGHQOGYPRKWRTDDAP 870

Db 933 VVPLDSMGNPRCDGHQOGYPRKWRTDDAP 962

RESULT 8

ID AAG67210 standard; Protein; 871 AA.

XX AAG67210;

AC AAG67210;

DT 13-NOV-2001 (first entry)

DE Amino acid sequence of a human stimulus-responsive channel protein.

DE Mechanical stimulus-responsive channel protein; kidney; cation channel;

KW hypertension; diabetes.

KW Homo sapiens.

OS WO200162915-A1.

PN 30-AUG-2001.

PD 23-FEB-2001; 2001WO-JP01354.

PF 25-FEB-2000; 2000JP-0048727.

PR (SNOW ) SNOW BRAND MILK PROD CO LTD.

PA Suzuki M, Ishibashi K;

PI WPI: 2001-550089/61.

DR N-PSDB; AAG67210.

XX Human or mouse-derived mechanical stimulus-responsive channel protein,

PT and encoding gene, for screening cation-channel activity enhancers or

PT inhibitors, or as diagnostics and treatments for hypertension and

PT diabetes.

XX Claim 9; Page 25-28; 35pp; Japanese.

PS The present sequence represents a mechanical stimulus-responsive channel

XX protein. The protein is expressed specially in the kidney and

CC non-selectively incorporates cations into cells respondent to a

CC mechanical stimulus. The mechanical stimulus-responsive channel protein

CC polynucleotide and polypeptide are useful in screening cation-channel

CC activity enhancers or inhibitors, as diagnostics or remedies for

CC diseases such as hypertension and diabetes, and also in drug development

CC to provide preventative treatment and remedies for the diseases.

XX Query Match

SQ Best Local Similarity 99.3%; Score 4546; DB 22; Length 871;

Matches 864; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPGEVAELPGDESGTTCGGEAFPLSSLANLFEDEGSLSPADASRPPG 60

Db 1 MADSSGPRAGPGEVAELPGDESGTTCGGEAFPLSSLANLFEDEGSLSPADASRPPG 60

Qy 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLYESSVVPKPKAPMDSLFYDGYTRHHSSDN 120

Db 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLYESSVVPKPKAPMDSLFYDGYTRHHSSDN 120

Qy 121 KRWKKTIIEKQSPKAPAPQPPPIKVFNRPIILFDIVSRGSTADLGLLPFLTHKKRL 180

Db 121 KRWKKTIIEKQSPKAPAPQPPPIKVFNRPIILFDIVSRGSTADLGLLPFLTHKKRL 180

Qy 181 TDEEFREPSTGKCLPKALLNLNGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240

Db 181 TDEEFREPSTGKCLPKALLNLNGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240

Qy 241 ALHIAIERCKHYVELLVAOGADVHAQARGRFQPKDEGGYFFGELPLSLAACTNPHI 300

Db 241 ALHIAIERCKHYVELLVAOGADVHAQARGRFQPKDEGGYFFGELPLSLAACTNPHI 300

Qy 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVKMYDLLLLKCARLPDS 360

Db 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVKMYDLLLLKCARLPDS 360

Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGFOHIIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Db 361 NLEAVLNNDGLSPLMMAAKTGKIGFOHIIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVFYINVSYLC 480

Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVFYINVSYLC 480

Qy 481 AMVIFLTAYIQPLEGTPPYPTVDYLRAGEVITLFTGVLFFFFTNFKDLFMKKCPGV 540

Db 481 AMVIFLTAYIQPLEGTPPYPTVDYLRAGEVITLFTGVLFFFFTNFKDLFMKKCPGV 540

Qy 541 NSLFDIGSFOLLYFIYSVLVISAALYLAGIEAYLAVMFALVGLMNNALYFTRGLKLTG 600

Db 541 NSLFDIGSFOLLYFIYSVLVISAALYLAGIEAYLAVMFALVGLMNNALYFTRGLKLTG 600

Qy 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTPSC 660

Db 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTPSC 660

Qy 661 RDSETFTFLDLFKLTIGMGDEMLSSSTKYPVVFILLVYIILFVLLNMLIALMGE 720

Db 661 RDSETFTFLDLFKLTIGMGDEMLSSSTKYPVVFILLVYIILFVLLNMLIALMGE 720

Qy 721 TVGOVSKESKHINKLOWATTILDIERSFPVFLKAFRSGBMTVVGKSSDGTDPDRRCFRV 780

Db 721 TVGOVSKESKHINKLOWATTILDIERSFPVFLKAFRSGBMTVVGKSSDGTDPDRRCFRV 780

Qy 781 DEYNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSNPDE 840

Db 781 DEYNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSNPDE 840

Qy 841 VVPLDSMGNPRCDGHQOGYPRKWRTDDAP 870

Db 841 VVPLDSMGNPRCDGHQOGYPRKWRTDDAP 870

RESULT 9

AAB86980

ID AAB86980 standard; Protein; 871 AA.

XX AAB86980;

XX 11-DEC-2001 (first entry)

DT Murine OTRPC4 protein.

DE OTRPC4; non-selective cation channel; antidiabetic; antihyperlipemic;

XX antihyperproteinemic; antihypertensive; cerebral; renal; osmolality;

KW osmo-sensor; diabetes; hyper-lipemia; hyper-proteinemia; hypertension;

stroke; renal insufficiency; shock; hyper-osmolality; hypo-osmolality;

transgenic animal; murine.

XX Mus sp.

OS DE10013296-Al.

PN 20-SEP-2001.

PD 17-MAR-2000; 2000DE-1013296.

PF 17-MAR-2000; 2000DE-1013296.

PR 17-MAR-2000; 2000DE-1013296.

XX

PA (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.  
XX Schults G, Plant T, Strotmann R, Harteneck C, Nunnenmacher K;  
PI WPI: 2001-590742/67.  
XX N-PSDB; AAI68414.  
DR New nucleic acid encoding the non-selective cation channel OTRPC4,  
XX useful for treating osmolality-associated disorders, e.g. diabetes  
PT comprises the modulation of activity -  
PT Example 1: Fig 2; 68pp; German.  
XX  
XX This invention describes a novel nucleic acid (I) which encodes a  
CC non-selective cation channel, OTRPC4 or its fragments, functional or  
CC allelic variants or subunits, variants of (I) within the degeneracy of  
CC the genetic code. The products of the invention have antidiabetic,  
CC antihyperlipemic, antihyperproteinemic, antihypertensive, cerebral and  
CC renal activity and are capable of modulating activity of OTRPC4, a  
CC non-selective cation channel that is regulated by changes in osmolality  
CC of the extracellular medium, i.e. it is an osmo-sensor for regulating  
CC cell volume. OTRPC4 is stimulated by a reduction in osmolality and is  
CC permeable for all cations, but with a preference for calcium.  
CC Polypeptides (II), encoded by (I), are useful for identifying  
CC (ant)agonists or modulators of (II), specifically blockers, activators  
CC or modulators of OTRPC4. (I) (or derived antisense molecules, vectors,  
CC and transfected cells) and (II) are useful for treating diabetes,  
CC hyper-lipemia or hyper-proteinemia, hypertension, stroke, renal  
CC insufficiency, shock or other pathological conditions associated with  
CC hyper- or hypo-osmolality. (I) is also used to prepare transgenic animals  
CC having an added, deleted or modified gene for OTRPC4. This sequence  
CC represents the murine OTRPC4 cation channel described in the method of  
CC the invention.  
XX  
XX Sequence 871 AA;

Query Match 95.8%; Score 4387; DB 22; Length 871;  
Best Local Similarity 95.2%; Pred. No. 0;  
Matches 828; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 1 MADSSGPRAGCEVAELPGDESGTGGEGAPFLSSLANLEFEGEDGSLSPADASRAGP 60  
DB 1 MADGDPRAAPEVAEPDGGESGTGGEGAPFLSSLANLEFEGEGSSLSLPVDSRAGP 60  
QY 61 GDCRPNLRMKFQGAFRGVNPNIDLLSTLYESSVPGPKAPMDSLFDTGRHSSDN 120  
DB 61 GDCRPNLRMKFQGAFRGVNPNIDLLSTLYESSVPGPKAPMDSLFDTGRHSSDN 120  
QY 121 KWRKKTIKOPQSPKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLLFLTHKKRL 180  
DB 121 KWRKKVVEKOPQSPKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLLFLTHKKRL 180  
QY 181 TDEFRPSTGKTCPLKALLNLNLRNDTIPVLLDIAERTGNRMREFINSFRDIYRGQT 240  
DB 181 TDEFRPSTGKTCPLKALLNLNLRNDTIPVLLDIAERTGNRMREFINSFRDIYRGQT 240  
QY 241 ALHAIATERRCKHVVLLVAGADVAQAARGFRFPQKDEGFFYFGELPLSLAECTNOPHI 300  
DB 241 SLHAIATERRCKHVVLLVAGADVAQAARGFRFPQKDEGFFYFGELPLSLAECTNOPHI 300  
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKFTVMYDILLKCARLPDPS 360  
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKFTVMYDILLKCARLPDPS 360  
QY 361 NLEAVNLNGLSLPMAAATGKIGIFQHIIRREVTEDTRHLSRKFWDWAYGVPYSSLYD 420  
DB 361 NLEAVNLNGLSLPMAAATGKIGIFQHIIRREVTEDTRHLSRKFWDWAYGVPYSSLYD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVPEINELLRDKWRKFCGAVSFYINVSYLEC 480  
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVPEINELLRDKWRKFCGAVSFYINVSYLEC 480  
QY 481 AMVIFTLAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTSIXDLFTKKCPGV 540

DB 481 AMVIFTLAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTSIXDLFTKKCPGV 540  
QY 541 NSLFDGSGFOLLXYFYISVLYVSAALYLAGIEAYLVAVFALVGNWALYFTFGLKLTG 600  
DB 541 NSLFDGSGFOLLXYFYISVLYVSAALYLAGIEAYLVAVFALVGNWALYFTFGLKLTG 600  
QY 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTYPSC 660  
DB 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTYPSC 660  
QY 661 RDSETFSTFLDLFLKLTIGMDLEMLSTKPYVFIILLVYIITLTVLLNMLIALMGE 720  
DB 661 RDSETFSTFLDLFLKLTIGMDLEMLSTKPYVFIILLVYIITLTVLLNMLIALMGE 720  
QY 721 TVGOVSKEKHINKLOWATILDIERSFPFLKAFRSGEMVTVGKSSDGTGPPDRRWCFRV 780  
DB 721 TVGOVSKEKHINKLOWATILDIERSFPFLKAFRSGEMVTVGKSSDGTGPPDRRWCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTHTVGRRLRRDSSVVRVVELNKNKNPDE 840  
DB 781 DEVNWSHWNQNLGIINEDPGKSEIYQYGFSTHTVGRRLRRDSSVVRVVELNKNKNSSADE 840  
QY 841 VVPLDSMGNPRCDGHQOQGYAPKWRDTDDAP 870  
DB 841 VVPLDLNLGNPCDGHQOQGYAPKWRDTDDAP 870  
RESULT 10  
AAG67209  
ID AAG67209 standard; Protein: 871 AA.  
XX  
AC AAG67209;  
XX  
DT 13-NOV-2001 (first entry)  
XX  
DE Amino acid sequence of a murine stimulus-responsive channel protein.  
XX  
KW Mechanical stimulus-responsive channel protein; kidney; cation channel;  
KW hypertension; diabetes.  
XX  
OS Mus sp.  
XX  
PN WO200162915-A1.  
XX  
PD 30-AUG-2001.  
XX  
PF 23-FEB-2001; 2001WO-JP01354.  
XX  
PR 25-FEB-2000; 2000JP-0048727.  
XX  
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX  
PI Suzuki M, Ishibashi K;  
XX  
DR WPI: 2001-550089/61.  
XX  
DR N-PSDB; AAH75192.  
XX  
PT Human or mouse-derived mechanical stimulus-responsive channel protein,  
PT and encoding gene, for screening cation-channel activity enhancers or  
PT inhibitors, or as diagnostics and treatments for hypertension and  
PT diabetes -  
XX  
PS Claim 3; Page 20-23; 35pp; Japanese.  
XX  
CC The present sequence represents a mechanical stimulus-responsive channel  
CC protein. The protein is expressed specially in the kidney and  
CC non-selectively incorporates cations into cells responsive to a  
CC mechanical stimulus. The mechanical stimulus-responsive channel protein  
CC polynucleotide and polypeptide are useful in screening cation-channel  
CC activity enhancers or inhibitors, as diagnostics or remedies for  
CC diseases such as hypertension and diabetes, and also in drug development  
CC to provide preventative treatment and remedies for the diseases.



XX	SQ	Sequence	871 AA;
XX	DT	16-OCT-2001 (first entry)	
DE	DE	Human vanilloid receptor VR3 isoform, VR3A-B-	
KW	KW	Human: vanilloid receptor; VR3; inflammatory condition; analgesic;	
KW	KW	intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;	
KW	KW	postmastectomy pain; complex regional pain syndrome; arthritis;	
KW	KW	rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;	
KW	KW	chronic obstructive pulmonary disease; irritable bowel syndrome;	
KW	KW	psoriasis; central nervous system disease; CNS; cancer;	
KW	KW	intestinal tract disorder; VR3A-B-	
XX	OS	Homo sapiens.	
XX	OS	WO200158945-A1.	
PX	PX	16-AUG-2001.	
PF	PF	01-FEB-2001; 2001WO-US03456.	
PR	PR	08-FEB-2000; 2000US-0500123.	
PA	PA	(ORTH ) ORTHO-WCNEIL PHARM INC.	
PI	PI	Dubin AE, Huvar A, Glass CA, Erlander MG;	
DR	DR	WPI: 2001-488969/53.	
XX	XX	N-PSDB: AAD12792.	
PT	PT	New human VR3 receptor useful for the treatment of disorders including	
XX	XX	cancers arthritis and pain -	
PS	PS	Claim 11; Fig 5; 104pp; English.	
CC	CC	The patent relates to human vanilloid receptor VR3 polynucleotide and	
CC	CC	polypeptide. Three isoforms of VR3 namely VR3A+B-, VR3A-B- and VR3A+B+	
CC	CC	have also been disclosed. The VR3 polypeptide is used to identify its	
CC	CC	modulators which are useful for the treatment of inflammatory conditions	
CC	CC	and for use as analgesics for intractable pain associated with	
CC	CC	postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex	
CC	CC	regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis),	
CC	CC	as well as ulcers, neurodegenerative diseases, asthma, chronic	
CC	CC	obstructive pulmonary disease, irritable bowel syndrome and psoriasis.	
CC	CC	The VR3 modulators are also useful for treatment of central nervous	
CC	CC	system (CNS) diseases, diseases of the intestinal tract, abnormal	
CC	CC	proliferation and cancer. The present sequence is human VR3 receptor	
CC	CC	isoform, VR3A-B-	
XX	XX	Sequence 811 AA;	
SQ	SQ	Query Match 92.2%; Score 4218; DB 22; Length 811;	
		Best Local Similarity 93.0%; Pred. No. 0;	
		Matches 809; Conservative 0; Mismatches 1; Indels 60; Gaps 1	
Qy	Qy	1 MADSSGPRAGGEVAELPGDESGETPGGEAFPLSLANLFEGEDGSLSPPADASRPAGP 60	
Db	Db	1 MADSSGPRAGGEVAELPGDESGETPGGEAFPLSLANLFEGEDGSLSPPADASRPAGP 60	
Qy	Qy	61 GDGRPNLRMKFQGAFKRGVNPIDLLLESTLYESSVVYGGPKAPMDSLFDYGYRRHSSDN 120	
Db	Db	61 GDGRPNLRMKFQGAFKRGVNPIDLLLESTLYESSVVYGGPKAPMDSLFDYGYRRHSSDN 120	
Qy	Qy	121 KRWKKTIIEKQSPKAPAPQPPIPILKVFNRPILFDIVSRGSTADLDGLLPILLTHKKRL 180	
Db	Db	121 KRWKKTIIEKQSPKAPAPQPPIPILKVFNRPILFDIVSRGSTADLDGLLPILLTHKKRL 180	
Qy	Qy	181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLDDIAERTGNRMREFINSPFRDIYYRGOT 240	
Db	Db	181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLDDIAERTGNRMREFINSPFRDIYYRGOT 240	
Qy	Qy	241 ALHAIATERCKHYVELLVAAQADVHAQAQRFFQPKDEGGYFYFGELPLSLAACACTNQPHI 300	
XX	XX	AAE06682 standard; Protein; 811 AA.	
AC	AC	AAE06682:	

RESULT 11  
AAE06682 .  
ID    AAE06  
XX  
AC    AAE06

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Db 241 ALHAIERRCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNPHI 300
Qy 301 VNYLTENPHKADMRRODSRGNTVLHALVAADNTRENTKFTVMYDLKLLKCARLPDS 360
Db 301 VNYLTENPHKADMRRODSRGNTVLHALVAADNTRENTKFTVMYDLKLLKCARLPDS 360
Qy 361 NLEAVLNDGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
Db 361 NLEAVLNDGLSPLMAAATG----- 381
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYL 480
Db 382 -----KIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYL 420
Qy 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 540
Db 421 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 480
Qy 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLGMNNAFYTRGLKLTG 600
Db 481 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLGMNNAFYTRGLKLTG 540
Qy 601 TYSIMIOKILFKDLFRLLVYLLFPMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Db 541 TYSIMIOKILFKDLFRLLVYLLFPMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 600
Qy 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPVVFVITLLVYIILTFVLLNMLIALMGE 720
Db 601 RDSETFTFLDLFKLTIGMDLEMLSTKYPVVFVITLLVYIILTFVLLNMLIALMGE 660
Qy 721 TVGVSKESKHIMKLOWATWILDIERSFPVFLKAFSGEMVTVGKSSDGTDPDRMCFV 780
Db 661 TVGVSKESKHIMKLOWATWILDIERSFPVFLKAFSGEMVTVGKSSDGTDPDRMCFV 720
Qy 781 DEVNWSHWNOLGIINDEPKNETYQYGFSTVGRRLRDRWSSVPRVVELNKNPNDE 840
Db 721 DEVNWSHWNOLGIINDEPKNETYQYGFSTVGRRLRDRWSSVPRVVELNKNPNDE 780
Qy 841 VVPLDSMGNPRCDGHOOGYPRKWRDTPAD 870
Db 781 VVPLDSMGNPRCDGHOOGYPRKWRDTPAD 810

RESULT 12
AAG63208
ID AAG63208 standard; Protein; 803 AA.
XX
AC AAG63208;
XX
XX 01-OCT-2001 (first entry)
XX
XX Amino acid sequence of novel human gene hcCh3.1.
XX
XX Human; hcCh3.1; hcCh3.2; hcCh4; cation channel; Alzheimer's disease;
XX ionic homeostatic dysfunction; central nervous system disorder;
XX stroke; neurological disorder; cardiac disorder; arrhythmia; diabetes;
XX chronic pain; hypercalcemia; hypocalcemia; hypercalcemia; hypocalcemia;
XX ion disorder; renal disease; liver disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Misc-difference 765
XX FT /note= "Asn encoded by AAG"
XX
XX W0200153348-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-US01804.
XX
XX 21-JAN-2000; 2000US-0177554.
XX
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PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Gaughan GT, Ramanathan CS;
XX
XX WPI; 2001-476103/51.
XX N-PSDB; AAH42583.
XX
XX New human cation channel nucleic acids and polypeptides, useful for
XX diagnosing and treating cation channel dysfunction, e.g. stroke or
XX neurological disorders (e.g. Alzheimer's disease), cardiac disorders or
XX diabetes
XX
XX Claim 24; Fig 2; 68pp; English.
XX
XX The present sequence represents a novel human polypeptide, designated
XX hcCh3.1. The specification also describes hcCh3.2 and hcCh4. hcCh are
XX human cation channels. The hcCh nucleic acid molecules and polypeptides
XX are useful for diagnosing and treating a variety of human disease
XX conditions that involve ion, particularly cation, channel dysfunction.
XX Specifically, the nucleic acids and polypeptides are useful for treating
XX human diseases, which involve calcium, sodium, potassium or other ionic
XX homeostatic dysfunction, e.g. central nervous system disorders (e.g.
XX stroke or neurological disorders such as Alzheimer's disease), cardiac
XX disorders (e.g. arrhythmia), diabetes, chronic pain, hypercalcemia,
XX hypocalcemia, hypercalcemia, hypocalcemia, or ion disorders
XX associated with renal or liver disease. In addition, the nucleic acid
XX molecules and polypeptides are useful in assays for identifying
XX compounds that modulate the expression of the hcCh genes and/or
XX activity of the hcCh gene products.
XX
XX SQ Sequence 803 AA;
XX
XX Query Match 92.1%; Score 4215; DB 22; Length 803;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 801; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 69 MKFGAFKRGKVPNPIDLESTLYESSVVPKAPMDSLFYGYTHSSDNKRKKII 128
Db 1 MKFGAFKRGKVPNPIDLESTLYESSVVPKAPMDSLFYGYTHSSDNKRKKII 60
Qy 129 EKQPSKAPAPQPPPIKLVFNRPILFDIVSRSTADLGLLFLTHKKRLDEEPREP 188
Db 61 EKQPSKAPAPQPPPIKLVFNRPILFDIVSRSTADLGLLFLTHKKRLDEEPREP 120
Qy 189 STGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQTAHAIER 248
Db 121 STGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQTAHAIER 180
Qy 249 RCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNPHIYNYLTENP 308
Db 181 RCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNPHIYNYLTENP 240
Qy 309 HKKADMRRODSRGNTVLHALVAADNTRENTKFTVMYDLKLLKCARLPDSNLEAVLNN 368
Db 241 HKKADMRRODSRGNTVLHALVAADNTRENTKFTVMYDLKLLKCARLPDSNLEAVLNN 300
Qy 369 DGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYDSSLDTCG 428
Db 301 DGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYDSSLDTCG 360
Qy 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAWIFTLT 488
Db 361 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAWIFTLT 420
Qy 489 AYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGVNSLFDGS 548
Db 421 AYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGVNSLFDGS 480
Qy 549 FOLLYFTYISVLIVSAALYLAGIEAYLAVMVFALVGLGMNNAFYTRGLKLTGYSIMIOK 608
Db 481 FOLLYFTYISVLIVSAALYLAGIEAYLAVMVFALVGLGMNNAFYTRGLKLTGYSIMIOK 540
Qy 609 ILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSCRDSETFTST 668
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|||||  
541 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVTPYPSCRDSEFST 600  
669 FLDLFLKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGTVGVQSKE 728  
601 FLDLFLKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGTVGVQSKE 660  
729 SKHIWKLOWATTILDIERSPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRVDEVNWSHW 788  
661 SKHIWKLOWATTILDIERSPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRVDEVNWSHW 720  
789 NONLGIINEDPGKNETYYGFSHTVGRLLRDRWSSVPRVVELNKNSPDDEVVPLDSM 848  
721 NONLGIINEDPGKNETYYGFSHTVGRLLRDRWSSVPRVVELNKNSPDDEVVPLDSM 780  
849 GNPRCDGHQOQYPRKWRDDAP 870  
781 GNPRCDGHQOQYPRKWRDDAP 802  
RESULT 13  
AAG63209  
ID AAG63209 standard; Protein: 743 AA.  
AC AAG63209;  
XX  
XX 01-OCT-2001 (first entry)  
XX  
XX Amino acid sequence of novel human gene hCch3.2.3.  
XX Human; hCch3.1; hCch3.2; hCch4; cation channel; Alzheimer's disease;  
KW ionic homeostatic dysfunction; central nervous system disorder;  
KW stroke; neurological disorder; cardiac disorder; arrhythmia; diabetes;  
KW chronic pain; hypercalcemia; hypocalcemia; hypercalciuria; hypocalciuria;  
KW ion disorder; renal disease; liver disease.  
XX  
XX Homo sapiens.  
XX  
XX Key . Location/Qualifiers  
FH Misc-difference 705  
FT /note= "Asn encoded by AAG"  
XX  
XX WO200153348-A2.  
XX 26-JUL-2001.  
XX  
XX 19-JAN-2001; 2001WO-US01804.  
XX  
XX 21-JAN-2000; 2000US-0177554.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Gaughan GT, Ramanathan CS;  
XX  
XX WPI; 2001-476103/51.  
XX N-PSDB; AA42584.  
XX  
XX New human cation channel nucleic acids and polypeptides, useful for  
PT diagnosing and treating cation channel dysfunction, e.g. stroke or  
PT neurological disorders (e.g. Alzheimer's disease), cardiac disorders or  
PT diabetes .  
XX  
XX Claim 24; Fig 4; 68pp; English.  
XX  
XX The present sequence represents a novel human polypeptide, designated  
CC hCch3.2. The specification also describes hCch3.1 and hCch4. hCch are  
CC human cation channels. The hCch nucleic acid molecules and polypeptides  
CC are useful for diagnosing and treating a variety of human disease  
CC conditions that involve ion, particularly cation, channel dysfunction.  
CC Specifically, the nucleic acids and polypeptides are useful for treating  
CC human diseases, which involve calcium, sodium, potassium or other ionic  
CC homeostatic dysfunction, e.g. central nervous system disorders (e.g.  
CC stroke or neurological disorders such as Alzheimer's disease), cardiac

disorders (e.g. arrhythmia), diabetes, chronic pain, hypercalcemia,  
CC hypocalcemia, hypercalciuria, hypocalciuria, or ion disorders  
CC associated with renal or liver disease. In addition, the nucleic acid  
CC molecules and polypeptides are useful in assays for identifying  
CC compounds that modulate the expression of the hCch genes and/or  
CC activity of the hCch gene products.  
XX  
SQ Sequence 743 AA;  
Query Match 84.5%; Score 3868; DB 22; Length 743;  
Best Local Similarity 92.5%; Pred. No. 0;  
Matches 742; Conservative 0; Mismatches 0; Indels 60; Gaps 1;  
QY 69 MKFCQAFKGVNPNIDLLSTLYESSVVPKPKAPMDSLFYGYRRHSSDNKRKKII 128  
DB 1 MKFCQAFKGVNPNIDLLSTLYESSVVPKPKAPMDSLFYGYRRHSSDNKRKKII 60  
QY 129 EKQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLPELLTHKKRLTDEEPREP 188  
DB 61 EKQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLPELLTHKKRLTDEEPREP 120  
QY 189 STGKTCLPKALLNLSNGRNDIPVLLDIAERTGNMREFINSPFRDIYRGOTALHAIER 248  
DB 121 STGKTCLPKALLNLSNGRNDIPVLLDIAERTGNMREFINSPFRDIYRGOTALHAIER 180  
QY 249 RCKHYVELLVAAQADVHAQARGRFQPKDEGGYFYFGLPLSLAECTNQHIVNYLTENP 308  
DB 181 RCKHYVELLVAAQADVHAQARGRFQPKDEGGYFYFGLPLSLAECTNQHIVNYLTENP 240  
QY 309 HKKADMRDROSGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDSNLEAVLNN 368  
DB 241 HKKADMRDROSGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDSNLEAVLNN 300  
QY 369 DGLSPLMAAATGIGIFQHIIRREVTDEDRHLRSKFKDWAYGPVYSSLYDLSLDTGC 428  
DB 301 DGLSPLMAAATGIGI----- 316  
QY 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAMVIFTLT 488  
DB 317 -----NRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAMVIFTLT 360  
QY 489 AYOPLGTPPYRTTVDYLRAGEVITLTGVLFFFTNKKDLFMKPCGVNSLFDIGS 548  
DB 361 AYOPLGTPPYRTTVDYLRAGEVITLTGVLFFFTNKKDLFMKPCGVNSLFDIGS 420  
QY 549 FOLLYFIYSLVIVSAALYLAGIEAYLAVMVYFALVGLGMNALYFTRGLKLTGYSIMIQK 608  
DB 421 FOLLYFIYSLVIVSAALYLAGIEAYLAVMVYFALVGLGMNALYFTRGLKLTGYSIMIQK 480  
QY 609 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVTPYPSCRDSEFST 668  
DB 481 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVTPYPSCRDSEFST 540  
QY 669 FLDLFLKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGTVGVQSKE 728  
DB 541 FLDLFLKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGTVGVQSKE 600  
QY 729 SKHIWKLOWATTILDIERSPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRVDEVNWSHW 788  
DB 601 SKHIWKLOWATTILDIERSPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRVDEVNWSHW 660  
QY 789 NONLGIINEDPGKNETYYGFSHTVGRLLRDRWSSVPRVVELNKNSPDDEVVPLDSM 848  
DB 661 NONLGIINEDPGKNETYYGFSHTVGRLLRDRWSSVPRVVELNKNSPDDEVVPLDSM 720  
QY 849 GNPRCDGHQOQYPRKWRDDAP 870  
DB 721 GNPRCDGHQOQYPRKWRDDAP 742  
RESULT 14  
AAE06683  
ID AAE06683 standard; Protein: 742 AA.

XX AC AAE06683;  
 XX DT 16-OCT-2001 (first entry)  
 XX DE Human vanilloid receptor VR3 isoform, VR3A+B+.  
 XX KW Human; vanilloid receptor; VR3; inflammatory condition; analgesic;  
 KW intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;  
 KW postmastectomy pain; complex regional pain syndrome; arthritis;  
 KW rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;  
 KW chronic obstructive pulmonary disease; irritable bowel syndrome;  
 KW psoriasis; central nervous system disease; CNS; cancer;  
 KW intestinal tract disorder; VR3A+B+.  
 XX OS Homo sapiens.  
 XX KW W0200158945-A1.  
 XX PD 16-AUG-2001.  
 XX PF 01-FEB-2001; 2001WO-US03456.  
 XX PR 08-FEB-2000; 2000US-0500123.  
 XX PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX PI Dubin AE, Huvar A, Glass CA, Erlander MG;  
 XX DR WPI; 2001-488969/53.  
 XX DR N-PSDB; AAD12793.  
 XX PT New human VR3 receptor useful for the treatment of disorders including  
 XX cancers arthritis and pain -  
 XX PS Claim 11; Fig 8; 104pp; English.  
 XX CC The patent relates to human vanilloid receptor VR3 polynucleotide and  
 CC polypeptide. Three isoforms of VR3 namely VR3A+B-, VR3A-B- and VR3A+B+  
 CC have also been disclosed. The VR3 polypeptide is used to identify its  
 CC modulators which are useful for the treatment of inflammatory conditions  
 CC and for use as analgesics for intractable pain associated with  
 CC postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex  
 CC regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis),  
 CC as well as ulcers, neurodegenerative diseases, asthma, chronic  
 CC obstructive pulmonary disease, irritable bowel syndrome and psoriasis.  
 CC The VR3 modulators are also useful for treatment of central nervous  
 CC system (CNS) diseases, diseases of the intestinal tract, abnormal  
 CC proliferation and cancer. The present sequence is human VR3 receptor  
 CC isoform, VR3A+B+.  
 XX SQ Sequence 742 AA;  
 Query Match 83.7%; Score 3829; DB 22; Length 742;  
 Best Local Similarity 100.0%; Pred. NO. 0;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADSSGPRAGGGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRPPG 60  
 DB 1 MADSSGPRAGGGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRPPG 60  
 QY 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLYESSVVPKPKAPMDSLFDTYRHHSSDN 120  
 DB 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLYESSVVPKPKAPMDSLFDTYRHHSSDN 120  
 QY 121 KRWKKTIEKQPSKAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180  
 DB 121 KRWKKTIEKQPSKAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180  
 QY 181 TDEEFREPSTGKTCPLKALLNLNSGRNDTIPVLLDIAERTGNMRETFNSFRDIYRGQT 240  
 DB 181 TDEEFREPSTGKTCPLKALLNLNSGRNDTIPVLLDIAERTGNMRETFNSFRDIYRGQT 240

QY 241 ALHIAIERRCKHYVELLVAGQADVHAQARGFFQPKDEGGYVFGELPLSLAACTNPHI 300  
 DB 241 ALHIAIERRCKHYVELLVAGQADVHAQARGFFQPKDEGGYVFGELPLSLAACTNPHI 300  
 QY 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLEPDS 360  
 DB 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLEPDS 360  
 QY 361 NLEAVLNDGLSPLMMAAKTGKIGIFOHIIIRREVTDEDTRHLSRKFCDWAYGVPYSSLYD 420  
 DB 361 NLEAVLNDGLSPLMMAAKTGKIGIFOHIIIRREVTDEDTRHLSRKFCDWAYGVPYSSLYD 420  
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLEC 480  
 DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLEC 480  
 QY 481 AMWIFTLTAYQPLEGTPPYRTTYDYLRLAGEVITLFTGVLFFFTNIDLPKMKKCPGV 540  
 DB 481 AMWIFTLTAYQPLEGTPPYRTTYDYLRLAGEVITLFTGVLFFFTNIDLPKMKKCPGV 540  
 QY 541 NSLFIDGSFOLLFYISVLVSAALYLAGIEAYLAVMVFALVGMNALLYFTRGKLTG 600  
 DB 541 NSLFIDGSFOLLFYISVLVSAALYLAGIEAYLAVMVFALVGMNALLYFTRGKLTG 600  
 QY 601 TYSIMTQKILFKDLFRFLVYLLFMIGYASALVSLNPNCANMKVCNEDQNTCTVPTPSC 660  
 DB 601 TYSIMTQKILFKDLFRFLVYLLFMIGYASALVSLNPNCANMKVCNEDQNTCTVPTPSC 660  
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 QY 721 TVGQVSKESKHIWKLQ 736  
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 AAU74936  
 ID AAU74936 standard; Protein; 602 AA.  
 XX AC AAU74936;  
 XX DT 23-APR-2002 (first entry)  
 DE Amino acid sequence of human vanilloid receptor-like protein 2b (VRL-2b).  
 KW Human; vanilloid receptor-like protein 2b; VRL-2b; hypertension;  
 KW ion-channel protein; pain; osteoarthritis; diabetic neuropathy;  
 KW neuralgia; nerve injury; neurodegeneration; stroke; inflammation;  
 KW asthma; allergy; urogenital disorder; incontinence; hypotension;  
 KW perivascular disease; VRL-related disease; receptor.  
 XX OS Homo sapiens.  
 XX PN EP1160254-A1.  
 XX PD 05-DEC-2001.  
 XX PF 25-MAY-2001; 2001EP-0304663.  
 XX PR 31-MAY-2000; 2000US-208156P.  
 XX PA (PFIZ ) PFIZER INC.  
 XX PI Shinjo K, Yabuuchi H;  
 XX DR WPI; 2002-084359/12.  
 XX DR N-PSDB; ABK14003.  
 XX PT New human vanilloid receptor-like proteins, useful for identifying  
 XX PT modulators for e.g. treating pain, also related nucleic acid

PS Claim 1; Page 21-22; 32pp; English.

Search completed: June 3, 2003, 19:54:19  
Job time : 76 secs

XX The present invention relates to a new polypeptide that has a sequence  
CC 871 amino acids (AAU74935) or 602 amino acids (AAU74936) long, or their  
CC variants, as defined in the specification. The polypeptide of the  
CC invention is deduced from a human nucleic acid 2749 base pairs (ABK14002)  
CC or 1900 base pairs (ABK14003) long, or their variants, also defined in  
CC the specification. The polypeptides of the invention, which are human  
CC vanilloid receptor-like (VRL) proteins, are used to identify specific  
CC modulators that are potentially useful for treating pain (of any origin),  
CC osteoarthritis, (diabetic) neuropathy, neuralgia, nerve injury,  
CC neurodegeneration, stroke, inflammation, asthma, allergy, urogenital  
CC disorders, incontinence, hypo- or hyper-tension and perivascular disease.  
CC The molecules of the invention can also be used to raise specific  
CC antibodies. The nucleic acid that encodes the polypeptide of the  
CC invention is useful for recombinant production of the protein and for  
CC preparing transgenic animal models. The polypeptide, antibody and nucleic  
CC acid of the invention are also useful as diagnostic agents for  
CC determining (susceptibility to) VRL-related diseases. The present amino  
CC acid sequence represents the human vanilloid receptor-like protein 2b  
CC (VRL-2b) of the invention.

XX  
SQ Sequence 602 AA;

Query Match 68.2%; Score 3121.5; DB 23; Length 602;  
Best Local Similarity 92.7%; Pred. No. 3.3e-290;  
Matches 601; Conservative 0; Mismatches 0; Indels 47; Gaps 1;

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DB 1 MREINSFPRDIYR----- 15

QY 283 YFGELPLSLAACTNQHIVNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFV 342  
DB 16 --GELPLSLAACTNQHIVNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFV 73

QY 343 TKMYDLLLLKCARLFPDSNLEAVLNDGLSPLMAAKTGKIGIFQHIIRREVTDEDTRHL 402  
DB 74 TKMYDLLLLKCARLFPDSNLEAVLNDGLSPLMAAKTGKIGIFQHIIRREVTDEDTRHL 133

QY 403 SRKFKWAYGVPVYSSLDLSDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLROK 462  
DB 134 SRKFKWAYGVPVYSSLDLSDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLROK 193

QY 463 WRKFGAVSFYINNVSYLCAMVIFLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGV 522  
DB 194 WRKFGAVSFYINNVSYLCAMVIFLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGV 253

QY 523 LFFETNIKDLPMKCPGVNSLFDGSPQLLYFIYSLVIVYSAALYLAGIEAYLAVMYFAL 582  
DB 254 LFFETNIKDLPMKCPGVNSLFDGSPQLLYFIYSLVIVYSAALYLAGIEAYLAVMYFAL 313

QY 583 VLGMNVALYFTRGLKLTGTYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPCANM 642  
DB 314 VLGMNVALYFTRGLKLTGTYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPCANM 373

QY 643 KVCNEDQTNCTVPTYPSCRSETFTFLDLFKLTIGMDLEMSSTKYPVVFILLVTV 702  
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DB 434 IILTFVLLNNLIALMGETGOVSKESHKWLQWATTILDIERSPFVFLKAFRSGEMV 493

QY 763 TVGKSSDGTDDRRCFRVDEYNWSHWNQNLGIINEDPGKNETYQYGFSTHVGRLRRDRW 822  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 19:53:03 ; Search time 18 seconds  
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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28: /cgn2\_6/ptodata/1/1aa/6Z\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	4218	92.2	811	4	US-09-500-123-9
3	3829	83.7	742	4	US-09-500-123-12
4	1845.5	40.3	843	4	US-09-235-451-25
5	1818	39.7	838	4	US-09-235-451-2
6	1818	39.7	838	4	US-09-132-316-3
7	1801	39.3	839	4	US-09-197-636-2
8	1800	39.3	839	4	US-09-197-636-8
9	1800	39.3	839	4	US-09-235-451-34
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11	1796	39.2	839	4	US-09-197-636-4
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27	134	2.9	1533	4	US-09-534-242-9

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#### ALIGNMENTS

#### RESULT 1

US-09-500-123-7

; Sequence 7, Application US/09500123

; Patent No. 6455278

; GENERAL INFORMATION:

; APPLICANT: Dubin, Adrienne E

; APPLICANT: Huvar, Arne

; APPLICANT: Erlander, Mark G

; APPLICANT: Glass, Charles A

; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor

; FILE REFERENCE: Human VR3

; CURRENT APPLICATION NUMBER: US/09/500,123

; CURRENT FILING DATE: 2000-02-08

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 871

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-500-123-7

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Db	121	KWRKXIIKQKQSPKAPAPQPP	ILKVFNRPI	LDIVSRGSTADLDGLP	FLTHKKRL 180	
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## RESULT 2

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US-09-500-123-9
; Sequence 9, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-9
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Query Match 92.2%; Score 4218; DB 4; Length 811;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 809; Conservative 0; Mismatches 1; Indels 60; Gaps 1;

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## RESULT 3

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US-09-500-123-12
; Sequence 12, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-12
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 VNYLTENPHKKADMRQDSRGNTVHALVAIADNTRENTKFTVMYDLLLLKCARLFPDS 360

QY 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKFEDWAYGVYSSLYD 420  
DB 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKFEDWAYGVYSSLYD 420

QY 421 LSSLDTCGGEASVLEILVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLEC 480  
DB 421 LSSLDTCGGEASVLEILVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLEC 480

QY 481 AMVIFTAYOPELECTPPYRTVDYLRAGEVITLFTGVLFETNFKDLMKPCGV 540  
DB 481 AMVIFTAYOPELECTPPYRTVDYLRAGEVITLFTGVLFETNFKDLMKPCGV 540

QY 541 NSLFDIGSQLLLYFYSVLVIVSAALYLAGIEAYLAVMVFALVGMNALLYTRGLKLTG 600  
DB 541 NSLFDIGSQLLLYFYSVLVIVSAALYLAGIEAYLAVMVFALVGMNALLYTRGLKLTG 600

QY 601 TYSIMQIKLFDLRFELVYLLFMIGYASALVSLNLANPCANMKVCNEDOTNCTVTPSC 660  
DB 601 TYSIMQIKLFDLRFELVYLLFMIGYASALVSLNLANPCANMKVCNEDOTNCTVTPSC 660

QY 661 ROSETFTFLDLFKLITIGMDLEMLSSSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
DB 661 ROSETFTFLDLFKLITIGMDLEMLSSSTKYPVVFILLVYIILTFVLLNMLIALMGE 720

QY 721 TVGQVSKESKHWWKQ 736  
DB 721 TVGQVSKESKHWWKQ 736

RESULT 4  
US-09-235-451-25  
; Sequence 25, Application US/09235451  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
; FILE REFERENCE: 9076/084CIP  
; CURRENT APPLICATION NUMBER: US/09/235,451  
; CURRENT FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461

; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 843  
; TYPE: PRT  
; ORGANISM: chicken  
US-09-235-451-25

Query Match 40.3%; Score 1845.5; DB 4; Length 843;  
Best Local Similarity 46.3%; Pred. No. 1.6e-163;  
Matches 399; Conservative 150; Mismatches 227; Indels 85; Gaps 23;

QY 41 EGEDGSLSPADASRPGPGDGRPNLRMKFOGAFKRGVNPIDLLLESTLY--ESSVVP 98  
DB 27 DGEDSAL--ETAD-----NLQTF---SNKVQPSKSNIFARRGRFVVG 64

QY 99 ---PKAPMDSLPDY-----GTYRHHSSDNKWRKKIIEKQ---QSPKAPQPPIL 146  
DB 65 DCDKMAPMDSFYQMDHLMAPSVIKPHANMERGKLHLLSTDSITGCSKA-----F 116

QY 147 KVENRPILFDIVSRGSTADLGLLFFLLTHKKRLTDEEFREPSTGKTCPLKALLNLSNGR 206  
DB 117 KFYDRRRIFDAVARGSTKDLDDLILYLNRTLKHLLTDEEFKEPETGKTCPLKALLNLSNGR 176

QY 207 NDTIPVLLDIAERTGNMREINSPFRDIYRGOTALHIAIERCKKHVVELLVAQGDVHA 266  
DB 177 NDTIPVLLDIAERTGNMREINSPFRDIYRGOTALHIAIERCKKHVVELLVAQGDVHA 236

QY 267 QARGRFQPK--KDEGGYFYFGEPLPLSLAACTNPHIYNTENPHKKADMRQDSRGNTVL 325  
DB 237 RACGEFPRKIKGPG--FYFGEPLPLSLAACTNOLCIVKLEENPYQAADIAAEDSMGMVL 295

QY 326 HALVAIADNTRENTKFTVMYDLLLLKCARLPPDSNLEAVLNNDGLSPLMAAATGKIGI 385  
DB 296 HTLVEIADNTRENTKFTVMYDLLLLKCARLPPDSNLEAVLNNDGLSPLMAAATGKIGI 355

QY 386 FOHITRREVTDETRHLSRKFEDWAYGVYSSLYDLSLDTGCEASVLEILVNSKIEN 445  
DB 356 FAYILRREIKDECHLSRKFETWAYGVYSSLYDLSLDTGCEASVLEILVNSKIEN 414

QY 446 RHEMLAVEPINELLRDKWRKFGAVSFYINVSYLEC--GTTPYPPY-- 502  
DB 415 RHEMLAVEPINELLRDKWRKFGAVSFYINVSYLEC--GTTPYPPY-- 474

QY 503 RTVDYLRAGEVITLFTGVLFETNFKDLMKPCGVNSLFDIGSQLLLYFYSVLVIV 562  
DB 475 HSTGEYFRVTGELSVGLGLYFFFRGIQ--YFVQRRESLKTLIVDSYSEVLFVHSLLS 533

QY 563 SAALYLAGIEAYLAVMVFALVGMNALLYTRGLKLTGTYSIMQIKLFDLRFELVYL 622  
DB 534 SVLVFCGQELVAVSWFSLAGWANMLYTRGFOQMGYISVYIAKMLIRDLRCRFVYL 593

QY 623 LFMIGYASALVSLNLANPCANMKVCNEDOTNCTVTPSCORSETEST-----FLDL 674  
DB 594 VELLGFSTAVVLIED-----DNEGQDTNSS--EYARCSHTKRGTSYNSLYTCLF 645

QY 675 KLITIGMDLEMLSSSTKYPVVFILLVYIILTFVLLNMLIALMGETVQVSKESKH 734  
DB 646 KFTIGMDLEFTENYRFSKVSFVILVYVILYIILTFVLLNMLIALMGETVQVSKESKH 705

QY 735 LQWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTTPDRRCFCFVDEYNWHSNNG 794  
DB 706 LQRPITILDIENSYNLCLRSRSGKRVLGITPDGDDYRNCFCFVDEYNWHSNNG 765

QY 795 INEDPG-----KNETYQYGFSGHTVGRLLRRDRWSVPRVVELKNSN----PDEV 844  
DB 766 INEDPGSGDLKRNPSY-----CIKPRVSGKGNKTLVPLLRDGSRRETPKLPESIK 820

QY 845 --LDSMGNPR--CDGHQOQYPR 862  
DB 821 PILEPYEPEDCETLKESLPK 841

```
RESULT 5
US-09-235-451-2
: Sequence 2, Application US/092335451
: GENERAL INFORMATION:
: APPLICANT: Julius David J.
: APPLICANT: Caterina, Michael J.
: APPLICANT: Brake, Anthony J.
: TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
: POLYPEPTIDES AND USES THEREOF
: TITLE OF INVENTION: 9076/084CIP
: CURRENT APPLICATION NUMBER: US/09/235.451
: CURRENT FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/072,151
: PRIOR FILING DATE: 1998-01-22
: PRIOR APPLICATION NUMBER: 08/915,461
: PRIOR FILING DATE: 1997-08-20
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 838
: TYPE: PRT
: ORGANISM: R. rattus
US-09-235-451-2

Query Match          39.7%; Score 1818; DB 4; Length 838;
Best Local Similarity 45.6%; Pred. No. 6e-161;
Matches 388; Conservative 141; Mismatches 222; Indels 100; Gaps 18;

QY 16 AELPGDESGTPGGE-----APLSSLANLFEDEGSLSPSPADA 54
DB 5 ASLSESESPPOENSCLDPPDRPNCKPPVPKPHIFTRSRTRLF-GKGDSEASPLDC 63
QY 55 SRPAGCGDGRPNLRMKFQGAFRGVPN-PIDLESTLYESSVVGPKKAPMDSLFYGTY 113
DB 64 PYEG-----GLASCIITVSSVL-----TIQPCDGP-----ASV 94
QY 114 RHSSDNKRWRKIIKQKQSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPFL 173
DB 95 RPSQDS-----VSAGEKPP--RLYDRRSIFDAVAQNCQELSLLPFL 136
QY 174 LTHKKRLTDEEFPSTGKTCPLKALLNLSNGRNDIPVLLDIAERTGNMREINSPFRD 233
DB 137 QRKKRLTDESEKDPETGKTCCLKAMLNHNGNDIALLLDVARKTDSLKQFVNASYTD 196
QY 234 IYRGOTALHIAIERCKHYVELLVQAQADVHAQARFPQKDEGGYFYFGEPLPLSLAA 293
DB 197 SYVGOTALHIAIERNNMTLVLLVENGADVQAANGDFKTKGRPGFYFGEPLPLSLAA 256
QY 294 CTNPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIAADNTRENTKFTVMYDILLKC 353
DB 257 CTNQLAIVKFLQNSWQPADISARDSVGNLHALVEADNTVDNTKFTVSMYNEILIG 316
QY 354 ARLPDSNLEAVLNQGLSPLMMAAKTGKIGIFQHIIRREVTDNTRHLSRKFKNAYGP 413
DB 317 AKLHPTLKEETNRKGLTALAASSGKIGVLAYTLQREIHEPECHLSRKFKNAYGP 376
QY 414 VYSLYDLSLDCGEEASVLEILVY-NSKIENRHEMLAVEPTNELLRDKWRKFGAVSFY 472
DB 377 VHSYDLSLDCIDTC-EKNSVLEIAYSSSETPNRHMVLLPELNRLLQDKWDRFVRIFY 435
QY 473 INVYSYLCAMVIFTLAYOPLGTPPYRTTV-DYLRAGEVITLFTGVLFFTNKID 531
DB 436 FNEFVYCLYMIIFTAAAYRPVPSGLPPYKLNVTGDFYRTVGEILSVSGVYFFRGIO- 494
QY 532 LFMKKCPGNSLFDIGSFOLLYFIYSLVIVSAALYAGIEAYLAVWVYFALVGNWALY 591
DB 495 YFQRRPSLKSLEVDYSSEILFFVQSLFVLVSVLYFSQREYKVASNVFSLAMGWNMLY 554
QY 592 FTRGLKLTGYSTMICKILFKDLFRLLVYLLFPMICYASALYSLLLPCANMKVCNEDQTN 651
DB 555 YTRGFOQMGIYAVMIENKMLRDLCRFMFVTLFVLFGFSTAVVTLI-----EDGKN 604

RESULT 6
US-09-132-316-3
: Sequence 3, Application US/091323168
: Patent No. 644440
: GENERAL INFORMATION:
: APPLICANT: Young, Paul E.
: APPLICANT: Ruben, Steven M.
: TITLE OF INVENTION: Vanilloid Receptor-2
: FILE REFERENCE: 1488.1110000
: CURRENT APPLICATION NUMBER: US/09/132,316B
: CURRENT FILING DATE: 1998-08-11
: EARLIER APPLICATION NUMBER: US 60/040,163
: EARLIER FILING DATE: 1997-03-07
: EARLIER APPLICATION NUMBER: PCT/US98/04493
: EARLIER FILING DATE: 1998-03-06
: NUMBER OF SEQ ID NOS: 67
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 3
: LENGTH: 838
: TYPE: PRT
: ORGANISM: Rattus norvegicus
US-09-132-316-3

Query Match          39.7%; Score 1818; DB 4; Length 838;
Best Local Similarity 45.6%; Pred. No. 6e-161;
Matches 388; Conservative 141; Mismatches 222; Indels 100; Gaps 18;

QY 16 AELPGDESGTPGGE-----APLSSLANLFEDEGSLSPSPADA 54
DB 5 ASLSESESPPOENSCLDPPDRPNCKPPVPKPHIFTRSRTRLF-GKGDSEASPLDC 63
QY 55 SRPAGCGDGRPNLRMKFQGAFRGVPN-PIDLESTLYESSVVGPKKAPMDSLFYGTY 113
DB 64 PYEG-----GLASCIITVSSVL-----TIQPCDGP-----ASV 94
QY 114 RHSSDNKRWRKIIKQKQSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPFL 173
DB 95 RPSQDS-----VSAGEKPP--RLYDRRSIFDAVAQNCQELSLLPFL 136
QY 174 LTHKKRLTDEEFPSTGKTCPLKALLNLSNGRNDIPVLLDIAERTGNMREINSPFRD 233
DB 137 QRKKRLTDESEKDPETGKTCCLKAMLNHNGNDIALLLDVARKTDSLKQFVNASYTD 196
QY 234 IYRGOTALHIAIERCKHYVELLVQAQADVHAQARFPQKDEGGYFYFGEPLPLSLAA 293
DB 197 SYVGOTALHIAIERNNMTLVLLVENGADVQAANGDFKTKGRPGFYFGEPLPLSLAA 256
QY 294 CTNPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIAADNTRENTKFTVMYDILLKC 353
DB 257 CTNQLAIVKFLQNSWQPADISARDSVGNLHALVEADNTVDNTKFTVSMYNEILIG 316
QY 354 ARLPDSNLEAVLNQGLSPLMMAAKTGKIGIFQHIIRREVTDNTRHLSRKFKNAYGP 413
DB 317 AKLHPTLKEETNRKGLTALAASSGKIGVLAYTLQREIHEPECHLSRKFKNAYGP 376
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Db 82 ITIQRPGDPTGARL-----LSODSVAASTEKTRLRY 113  
QY 150 NRPILFDIVSRGSTADLGLPFLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT 209  
Db 114 DRRSFEVAQNOCODESLLFLQKSKKHLTDNEFKDPETKCTCLLKAMLNLDGQNTT 173  
QY 210 IPVLDDIABRTGNMREFINSPPRDIYRGOTALTHAIERRCKHYVELLVAAQADVHAQAR 269  
Db 174 IPLLLEIARQOTSLKELVNASYDSYKGTOTALTHAIERNMALVTLLVENGADVQAAAH 233  
QY 270 GRFPQKDEGGYFEGELPLSLAACNQHPIVNYLTENPHKKADMRROSGRNTVULHALV 329  
Db 234 GDFFKTKRPGFYFEGELPLSLAACNQLGIVKFLQNSWQOTADISARSDVGNVTULHALV 293  
QY 330 ATADNTRENTKVTMYDLKLCARLPDSNLEAVLNNDGLSPLMMAAKTKIGIFOHI 389  
Db 294 EVADNTADNTKVTSMYNEILLGAKLHPTLKEELTNKKGMPLAALAGTCKIGVLA 353  
QY 390 IREVTDETRHLSRKFKDWAYGPVYSSLYDLSLDTGCEASVLEILVY-NSKIENRHE 448  
Db 354 LQREIQEPECHLSRKFKTEWAYGPVHSSLYDLSIDTC-EKNSVLEVIAYSSSETPNRHD 412  
QY 449 MLAVEPINELLRDKWRKFCGAVSYINVSYLCAWIFLTATYQPLEGTPPYRTTVDY 508  
Db 413 MLLVPELRLQDKWDRFVKRIFYFNFLVCLYMIIFTMAAYRVPDGLPPFKMEKTGDY 472  
QY 509 LRLAGEVITLFTGVLFFFFTNIKDFMKKCPGVNSLFDIGSFOLLYFIYSVLVISAALV 568  
Db 473 FRVTGEILSVLGGVYFFFRGIO-YFLQRRPSMKTFLVDYSYSEMLFFLOSLFMTATVLYF 531  
QY 569 AGIEAYLAVMVFALVGLMGNALYFTRGLKLTGYTSIMQIKILFKDLFRLLVYLLFMIGY 628  
Db 532 SHLKEYVASMVFSLALGNTMMLYTRGFQOMGIYAVMIEKMLRDLCRFMFYVVFVLF 591  
QY 629 ASALVSLNPNCAKMKVCNEDQNTCTVPTY-----PSCRSET-----FSTFLDLDFK 675  
Db 592 STAVVTLI-----EDKNDLSPSESTSHRWGPACRPPDSSYNSLYST-CLELFK 640  
QY 676 LTIGMDLEMSSTKYPVVFIILVYIILTVLILFVLLNMLIALMGETVGVSKESKHIWKL 735  
Db 641 FTIGMGDLFEYNDYFKAFFIILAYVILYVILLNMLIALMGETVGVSKESKHIWKL 700  
QY 736 QWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDPDRRCFRVDEVNWHSNQNGLII 795  
Db 701 QRAITILDTEKSFCLKMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDENVNTWNTNNGII 760  
QY 796 NEDPKNE-TYOYGYGFSHTVGLRLRRDRWS--SVWPRVVELN----KNSNPDEV 841  
Db 761 NEDPNCCEGVKRTLSFSLRSSRVSGRHKMKNFALVPLLRASARDRQSAQPEV 813

## RESULT 10

US-09-533-220A-2  
; Sequence 2, Application US/09533220A  
; Patent No. 6406908  
; GENERAL INFORMATION:  
; APPLICANT: McIntyre, Peter  
; APPLICANT: James, Iain Fraser  
; TITLE OF INVENTION: Human Vanilloid Receptor  
; FILE REFERENCE: 4-30875A  
; CURRENT APPLICATION NUMBER: US/09/533,220A  
; CURRENT FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9507097.1  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 1.30  
; SEQ ID NO 2  
; LENGTH: 839  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-533-220A-2

Query Match 39.3%; Score 1799; DB 4; Length 839;

Best Local Similarity 44.9%; Pred. No. 3.6e-159;  
Matches 374; Conservative 155; Mismatches 223; Indels 81; Gaps 15;  
QY 49 PSPADASRPAAGCDGRPNL-----RMKFOG-----AFRKGVPNPIDLLLES--TLYESSV 95  
Db 22 PDPLDGDPNRSPPAKPOLSTAKSRTRLFCKGDSSEAFVDCPHEGEGLDSCPTIVPSV 81  
QY 96 V-----PGPKAPDMSLFDYGTYRHHSSDNKRWRKIIKEKQPSKAPAPQPPPTLVK 149  
Db 82 ITIQRPGDPTGARL-----LSODSVAASTEKTRLRY 113  
QY 150 NRPILFDIVSRGSTADLGLPFLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT 209  
Db 114 DRRSFEVAQNOCODESLLFLQKSKKHLTDNEFKDPETKCTCLLKAMLNLDGQNTT 173  
QY 210 IPVLDDIABRTGNMREFINSPPRDIYRGOTALTHAIERRCKHYVELLVAAQADVHAQAR 269  
Db 174 IPLLLEIARQOTSLKELVNASYDSYKGTOTALTHAIERNMALVTLLVENGADVQAAAH 233  
QY 270 GRFPQKDEGGYFEGELPLSLAACNQHPIVNYLTENPHKKADMRROSGRNTVULHALV 329  
Db 234 GDFFKTKRPGFYFEGELPLSLAACNQLGIVKFLQNSWQOTADISARSDVGNVTULHALV 293  
QY 330 ATADNTRENTKVTMYDLKLCARLPDSNLEAVLNNDGLSPLMMAAKTKIGIFOHI 389  
Db 294 EVADNTADNTKVTSMYNEILLGAKLHPTLKEELTNKKGMPLAALAGTCKIGVLA 353  
QY 390 IREVTDETRHLSRKFKDWAYGPVYSSLYDLSLDTGCEASVLEILVY-NSKIENRHE 448  
Db 354 LQREIQEPECHLSRKFKTEWAYGPVHSSLYDLSIDTC-EKNSVLEVIAYSSSETPNRHD 412  
QY 449 MLAVEPINELLRDKWRKFCGAVSYINVSYLCAWIFLTATYQPLEGTPPYRTTVDY 508  
Db 413 MLLVPELRLQDKWDRFVKRIFYFNFLVCLYMIIFTMAAYRVPDGLPPFKMEKTGDY 472  
QY 509 LRLAGEVITLFTGVLFFFFTNIKDFMKKCPGVNSLFDIGSFOLLYFIYSVLVISAALV 568  
Db 473 FRVTGEILSVLGGVYFFFRGIO-YFLQRRPSMKTFLVDYSYSEMLFFLOSLFMTATVLYF 531  
QY 569 AGIEAYLAVMVFALVGLMGNALYFTRGLKLTGYTSIMQIKILFKDLFRLLVYLLFMIGY 628  
Db 532 SHLKEYVASMVFSLALGNTMMLYTRGFQOMGIYAVMIEKMLRDLCRFMFYVVFVLF 591  
QY 629 ASALVSLNPNCAKMKVCNEDQNTCTVPTY-----PSCRSET-----FSTFLDLDFK 675  
Db 592 STAVVTLI-----EDKNDLSPSESTSHRWGPACRPPDSSYNSLYST-CLELFK 640  
QY 676 LTIGMDLEMSSTKYPVVFIILVYIILTVLILFVLLNMLIALMGETVGVSKESKHIWKL 735  
Db 641 FTIGMGDLFEYNDYFKAFFIILAYVILYVILLNMLIALMGETVGVSKESKHIWKL 700  
QY 736 QWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDPDRRCFRVDEVNWHSNQNGLII 795  
Db 701 QRAITILDTEKSFCLKMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDENVNTWNTNNGII 760  
QY 796 NEDPKNE-TYOYGYGFSHTVGLRLRRDRWS--SVWPRVVELN----KNSNPDEV 841  
Db 761 NEDPNCCEGVKRTLSFSLRSSRVSGRHKMKNFALVPLLRASARDRQSAQPEV 813

## RESULT 11

US-09-197-636-4  
; Sequence 4, Application US/09197636  
; Patent No. 6239267  
; GENERAL INFORMATION:  
; APPLICANT: DUCKWORTH, DAVID  
; APPLICANT: HAYES, PHILIP  
; APPLICANT: MEADOWS, HELEN  
; APPLICANT: DAVIS, JOHN  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia

```

: STREET: P.O. Box 980
: CITY: Valley Forge
: STATE: PA
: COUNTRY: US
: ZIP: 19482-0980
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/197,636
: FILING DATE: 23-NOV-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: UK 9805137.8
: FILING DATE: 12-MAR-1998
: APPLICATION NUMBER: UK 9815791.0
: FILING DATE: 21-JUL-1998
: APPLICATION NUMBER: UK 9819278.4
: FILING DATE: 03-SEP-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Prestia, Paul F
: REGISTRATION NUMBER: 23,031
: REFERENCE/DOCKET NUMBER: GP-30075
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 601-407-0700
: TELEFAX: 610-407-0701
: TELEX: 846169
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 839 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-197-636-4

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Query Match          39.2%; Score 1796; DB 4; Length 839;
Best Local Similarity 44.8%; Pred. No. 6.9e-159;
Matches 373; Conservative 156; Mismatches 223; Indels 81; Caps 15;

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QY 49 PSPADSRPAGDGRNL-----RMKFGQ-----AFKGVNPIDLLFS--TLYESSV 95
DB 22 PDLGDGPNRPAPQQLSTAKSRFLFGKSEAFVDCPHEGELSCPTITVSPV 81
QY 96 V-----PGPKAPMDSLFDYGYRHHSSDNKRWRKKIIEKQPSKAPAPQPPILKVF 149
DB 82 ITIORPCDGTGARL-----LSQDSVAASTEKTLRLY 113
QY 150 NRPILEDIVSRGTADLGLLPPELLTHKKRLTDEEPREPSTGKTCPLKALLNSGRNDT 209
DB 114 DRSIFEAVQNNCODLESLLFLQSKKHXTDNEFKDPETGKTCLLKAMLNLDGQNTT 173
QY 210 IPVLLDTAERTGNMREINSPERDIYRGOTALHIAIERCKHYVELLVAAQADVHAQAR 269
DB 174 IPLLLETARTDLSKELVNAXYTDYXKGTQALHIAIERRMALVTLVLLVENGADVOAAH 233
QY 270 GREFFQKDEGGYFYFGLPLSLAACTNQPHIVNLTENPHKKADMRRQDSRGNTVHLAV 329
DB 234 GDFEKKTKRPGFYFGLPLSLAACTNQLGIVKFLQNSQWADISARDSVGNVTVLHALV 293
QY 330 AIADNTRENTKFTVKHYDLLLLKARLFPDSNLEAVLNNDGLSPLMMAKTGKIGIFQHI 389
DB 294 EVADNTADNTKFTSYMNEILGAKLHPTLKLEELTNKKGMTPLAAGTGKIGVLAYI 353
QY 390 IREVDTEDETRHLSRAFKWAYGPVYSSLYDLSLDTCGEASVLEILVY-NSKIEHRH 448
DB 354 LOREIOBPCRHLRSKFTWAYGPHVSSLYDLSCIDTC-EKNSVLEIAYISSETPNRHD 412
QY 449 MLAVEPINELLRDKRKFAGVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYRYRTVDY 508
DB 413 MLLVEPLNRLQDKWRFKRIEYFNFLVYCLYMIIFTMAAYYRPVDGLPPFKMEXTGDY 472

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QY 509 LRLAGEVITLTGTGLFFFTNIKDLPMKCPGVNSLFDGCSFQLLYFIYVULVIVSAALYL 568
DB 473 FRVTGEILSLVGGVYFFFRGIQ-YFLQRRPSMKTLFVDSYSEMFLFLQSLFMLATVVLVYF 531
QY 569 AGTEAYLAVVYFALVGLGMNALYFTRGKLTGTYSIMQKTLFKDLPFRFLVLLYLLFMIGY 628
DB 532 SHLKEYVASWVSLALGWTNMLYTRGQFMGIYAVMIEKMLRDLGRFMFVYVFLVFGF 591
QY 629 ASALVSLNFCANMKVCNEDQTNCTVPTY-----PSCRDSET-----FSTFLDLDFK 675
DB 592 STAVVTLI-----EDGKNDLSPSESTSHRWGRGPACRPDPSSYNSLYST-CLELFFK 640
QY 676 LTGMGLEMLSSTKYPVVIILLYIITLVLLNMLIALMGETVGVQVSKESKHVWL 735
DB 641 FTIGMGDLEFTENYDFKAVFIILLAYVILTYILLNMLIALMGETVYKIAQESKNVWL 700
QY 736 QWATTILDIERSFPVFLRKAFRSGEMVYVCKSGSDGTPDRRCFVRVDEVNKNHNONLGII 795
DB 701 ORAITILDTKSEFLKCMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNNTWNTNVGII 760
QY 796 NEDPGKNE-TYQYGFSTHTVGLRRDRWS--SVVPRVVELN---KNSNPDEV 841
DB 761 NEDPGNCEGVKRTLSPSLRSRVSGRHKNFALVPLLRASARDROSAQPEEV 813

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## RESULT 12

```

US-09-235-451-4
: Sequence 4, Application US/092335451
: GENERAL INFORMATION:
: APPLICANT: Julius, David J.
: APPLICANT: Caterina, Anthony J.
: TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
: TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
: TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
: FILE REFERENCE: 9076/084CIP
: CURRENT APPLICATION NUMBER: US/09/235,451
: CURRENT FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/072,151
: PRIOR FILING DATE: 1998-01-22
: PRIOR APPLICATION NUMBER: 08/915,461
: PRIOR FILING DATE: 1997-08-20
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 761
: TYPE: PRT
: ORGANISM: R. rattus
: US-09-235-451-4

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Query Match          32.7%; Score 1497.5; DB 4; Length 761;
Best Local Similarity 43.6%; Pred. No. 4.8e-131;
Matches 336; Conservative 123; Mismatches 247; Indels 65; Caps 14;
QY 103 PMDSLFQDYGYRHHSSDNKRWRKKIIEKQPSKAPAPQPPILKLVNRPILFDIVSRGS 162
DB 34 PMSFPQ--REDNRNSPQIKVNFIRKPPKNTSAPSOQEP---DRFDRDLFSVSVRGV 88
QY 163 TADLDGLPLLPKRLTDEEPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGN 222
DB 89 PEELTGLLEVLWNYSKYLTDTSAYTEGSTGKTCMLKAVLNLODGVNACIMPLLOIDKDSGN 148
QY 223 MREFINSPFDIYYRGOTALHIAIERCKHYVELLVAAQADVHAQAGRFPQPKDEGGYF 282
DB 149 PKPLVNAQCTDEFYQGSALHIAIERKSLQCVKLLVENGADVHLRACGRFPQ-KHQCTCF 207
QY 283 YFCEPLSLAACTNQPHIVNLTENPHKKADMRRQDSRGNTVHLVALVAIADNTRKNTKFV 342
DB 208 YFCEPLSLAACTKQMDVVTYLLLENPHQPSLEATDSLGNVTYHLVALVADNSPENSALV 267
QY 343 TKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAKTGKIGIFQHIIRREVTEDETRHL 402

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Db 268 IHMYDGLQWARGCTVTOLEISNMQGLTPLKLAKEGKIEIFRHILOREFSG-PYOPL 326  
QY 403 SRKFKDWAYGPVSSLYDLSSLDTCGEASVLEIILVYNSKIENRHEMLAVEPINELLROK 462  
Db 327 SRKFEMWCYGPVRSYDLSSVDS-WEKNSVLEIITAFHCKSPRRHRMVLEPLNKLQEK 385  
QY 463 WRKFGAVSYINVSYLCAWVITITAYQPLEGPPYP--YRTTVDYLRAGEVITLFT 520  
Db 386 WDRL-VSRFFNFACVLYVMFTVAVHOPSLDQPAIPSSKATTFESMLLGHILILG 444  
QY 521 GV-----LFFFTNKLKPMKCPGVNSLFDGSGQLLYFIYSLVIVSAALYLAGIEAY 574  
Db 445 GYLLGLQWYFWR-RRUF-----IWISFMDSYFEILFQALLTVLSQVLRMETEWY 497  
QY 575 LAVMYFALVGLWGNALYFTRGLKLTGTSIMQKILFKDLFRLLVYLLFMIGYASALS 634  
Db 498 LPALLVSLVGLWNLVYTRGPHGTGIYSVMQKVLRLDLLFLLVYLVFLGFAVALVS 557  
QY 635 LNPCKANKVCNEDQTNCTVTPYPCRSDETSF-----LDLFKLTIGMDLEMLSS 688  
Db 558 LSREARSPKA--PEDNNSTVTEQTVGOEPEAPYRSILDASLELFKFTIGMELAFQEQ 615  
QY 689 TRYPVVFILLVYIILFVLLNMLIALMGETVQVSKESKHINKLOWATTILDIERSF 748  
Db 616 LRFRGVULLLLAYVLLTYVLLNMLIALMSETVNHVADNSWINKLOKAIISVLEMENGY 675  
QY 749 PVFLKAKRSGEMVTVGKSSDGTDPDRWCFRVDEVNWSHWNONLGIINEDP----- 800  
Db 676 WWCRRKKHREGLLKVGTRGDTGTPDERWCFRVEEVNWAAREKTLTSLSDPGSGGITGNK 735  
QY 801 KNETYQYGFSTVGLRRDRWSSVYVVELNKNPNDEVVVPLDSMGNP 851  
Db 736 KNPT-----SKPGKNSASEDHLPLQVLQSP 761

## RESULT 13

US-09-132-316-2  
; Sequence 2, Application US/09132316B  
; Patent No. 6444440  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul E.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Vanilloid Receptor-2  
; FILE REFERENCE: 1488.1110000  
; CURRENT APPLICATION NUMBER: US/09/132,316B  
; CURRENT FILING DATE: 1998-08-11  
; EARLIER APPLICATION NUMBER: US 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 889  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-132-316-2

Query Match 32.2%; Score 1474.5; DB 4; Length 889;  
Best Local Similarity 41.4%; Pred. No. 8.8e-129;  
Matches 340; Conservative 118; Mismatches 258; Indels 105; Gaps 14;  
QY 20 GDESTPGGEAFPLSSLANLEFEGDGLSPSPADASRAGP----- 60  
Db 94 GHRRAKRGKGTPLTSPSAQRSLWDRAMPPPPRMTSPSSSPVRLTLDGGOEDSEADR 153  
QY 61 -----GDRPNLRMKFQCAFRKGVDPNPIDLLESTLYESSVVPKPKAPMDSLFDVGYVRH 115  
Db 154 KGLDFGSLPWPMSQFQEDRKFP----- 178  
QY 116 HSSDNKRWRKKIIEKQSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLPFLIT 175  
Db 179 QIRVNLNRYK-----GTGASQDP--NREDRDLFNVAHSVGVPEDLAGLPEYLSK 226

QY 176 HKKRLTDEFRPSTGKTCPLKALLNSNRNDTIPVLLDIAERTGNREFINSPRDIY 235  
Db 227 TSKYLTDSYETSGTGKTCMLKAVLNKGVNACILPLLOIDRDSNPOPLVNAQCTDDY 286  
QY 236 YGQATALHAIERRCKHYVELLYVAOGADVHAQARFFQPKDEGGYFYFGEPLSLAACT 295  
Db 287 YRGHSALHAIIEKRSLOQCVKLVENCANVHARACGRFQ--KGQCTCFYFGEPLSLAACT 345  
QY 296 NQPHVNLVLTENPHKADMRRODSRGNTVHLVATADTNTRENTKVTVMYDILLKLCAR 355  
Db 346 KQMDVVSYLLENPHOPASLOQSDSGNTVHLVAMISDMSAENALVTSYDGLLOAGAR 405  
QY 356 LFPDSNLEAVLNNDGLSPLMAAKTGKIGIFQIIRREVTDETRHLSRKFKDWAYGPVY 415  
Db 406 LCPTVOLEDIRNLQDLTPLKLAKEGKIEIFRHILOREFS--GLSHLSRKFTWCYGPVR 463  
QY 416 SSLYDSSLDTCGEASVLEIILVYNSKIENRHEMLAVEPINELLRDKRKFAGVSYINV 475  
Db 464 VSLYDLASVDSC--EENSVELEIITAFHCKSPRRHRMVVLEPLNKLQAKWDL-IPKFFLNF 521  
QY 476 VSYLCAMVITLTAYQOP--LEGTPPYPTTVDYLRAGEVITLFTGVLFFFFTNKKDLEM 534  
Db 522 LCNLYMFTTAVAHQPTLKAAPHLKAEVGNMMLTGHILILGGLVLLVQQLW-YEW 580  
QY 535 KPCPGVNSLFDGSGQLLYFIYSLVIVSAALYLAGIEAYLAVMYFALVGLWGNALYFTR 594  
Db 581 RRVHVTWISFIDSYFEILFQALLTVYSQVLCFLAEIHWYLLPLVLSALVGLWNLVYTR 640  
QY 595 GUKLTGTSIMQKILFKDLFRLLVYLLFMIGYASALSINLPCANMKVCNEDQTNCTV 654  
Db 641 GFQHTGIYSVMQKVLRLDLLFLLIYLVFLGFAVALVS-----SQEAMRPEA 690  
QY 655 PTPYPCRS-----ETSFEL-----LDLFKLTIGMDLEMLSSYKPVVFIIL 698  
Db 691 PTGPNATESVPMQGOEDGNGAQVRGILEASLELFKFTIGMELAFQEQHLFRGMVLLL 750  
QY 699 LVYTIILFVLLNMLIALMGETVQVSKESKHINKLOWATTILDIERSFPVFLRKAFRS 758  
Db 751 LLAYVLLYIYLLNMLIALMSETVNSVATDSINKKLOKAIISVLEMENGY--WCCRKKQRA 809  
QY 759 GEMVTVGKSSDGTDPDRWCFRVDEVNWSHWNONLGIINEDP 799  
Db 810 GVMLTVGTPKDPGSDPDERWCFRVEEVNWSWASQETLPTLCBDP 850

## RESULT 14

US-09-235-451-36  
; Sequence 36, Application US/09235451  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 9076/084CIP  
; CURRENT APPLICATION NUMBER: US/09/235,451  
; CURRENT FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 764  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-235-451-36

Query Match 32.1%; Score 1467; DB 4; Length 764;  
Best Local Similarity 43.1%; Pred. No. 3.5e-128;





Db 667 FRVEYNWASWEOTLPTLCEDP 688

Search completed: June 3, 2003, 19:56:29  
Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run On: June 3, 2003, 19:54:28 ; Search time 28 seconds  
(without alignments)  
3145.165 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSSGPRAGPCEVAELPG.....PRCDGHQGYPRKWRDADP 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4573	99.9	871	9	US-10-027-828-4
2	4573	99.9	871	9	US-10-000-823-7
3	4571	99.9	871	9	US-10-027-828-2
4	4571	99.9	871	9	US-10-090-215-7
5	4546	99.3	871	9	US-10-227-255A-3
6	4378	95.7	871	9	US-10-027-828-11
7	4374	95.6	871	9	US-10-227-255A-1
8	4372	95.5	871	9	US-10-027-828-10
9	4371	95.5	871	9	US-10-027-828-8
10	4371	95.5	871	9	US-10-027-828-9
11	4334.5	94.7	870	9	US-10-027-828-13
12	4218	92.2	811	9	US-10-090-215-9
13	4199	91.7	803	10	US-09-764-367A-8
14	4138	90.4	792	10	US-09-764-367A-2
15	4127.5	90.2	830	9	US-10-027-828-6
16	3853	84.2	743	10	US-09-764-367A-11
17	3831.5	83.7	852	9	US-10-027-828-15
18	3829	83.7	742	9	US-10-090-215-12
19	3783.5	82.7	734	10	US-09-764-367A-4

20	2307	50.4	461	9	US-10-027-828-5	Sequence 5, Appli
21	2059.5	45.0	420	9	US-10-027-828-7	Sequence 7, Appli
22	1845.5	40.3	843	9	US-09-978-303-25	Sequence 25, Appl
23	1818	39.7	838	9	US-10-137-316-3	Sequence 3, Appli
24	1818	39.7	838	9	US-09-978-303-2	Sequence 2, Appli
25	1811.5	39.6	707	9	US-10-027-828-17	Sequence 17, Appli
26	1801	39.3	839	10	US-09-824-258-2	Sequence 2, Appli
27	1800	39.3	839	9	US-10-000-823-5	Sequence 5, Appli
28	1800	39.3	839	9	US-09-978-303-34	Sequence 34, Appli
29	1800	39.3	839	10	US-09-824-258-8	Sequence 8, Appli
30	1799	39.3	839	9	US-10-128-853-2	Sequence 2, Appli
31	1796	39.2	839	10	US-09-824-258-4	Sequence 4, Appli
32	1745	38.1	829	10	US-09-764-367A-7	Sequence 7, Appli
33	1497.5	32.7	761	9	US-09-978-303-4	Sequence 2, Appli
34	1474.5	32.2	889	9	US-10-137-316-2	Sequence 6, Appli
35	1467	32.1	764	9	US-10-000-823-6	Sequence 36, Appli
36	1467	32.1	764	9	US-09-978-303-36	Sequence 4, Appli
37	1467	32.1	764	10	US-09-828-466-4	Sequence 18, Appli
38	1459.5	31.9	665	9	US-10-027-828-18	Sequence 5, Appli
39	1454.5	31.8	764	10	US-09-828-466-5	Sequence 6, Appli
40	1445.5	31.6	790	9	US-10-011-582-6	Sequence 10, Appli
41	1438	31.4	761	9	US-10-011-582-10	Sequence 9, Appli
42	1436	31.4	760	10	US-09-764-367A-9	Sequence 2, Appli
43	1429.5	31.2	724	9	US-10-011-582-2	Sequence 2, Appli
44	1410.5	30.8	720	9	US-10-000-823-2	Sequence 4, Appli
45	1410.5	30.8	745	9	US-10-000-823-4	

ALIGNMENTS

RESULT 1

US-10-027-828-4

; Sequence 4, Application US/10027828

; Publication No. US20030013650A1

; GENERAL INFORMATION:

; APPLICANT: Liedtke, Wolfgang

; APPLICANT: Heller, Stefan

; APPLICANT: Hudspeth, Albert J.

; APPLICANT: Friedman, Jeffrey M.

; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC

; TITLE OF INVENTION: IT, AND USES THEREOF

; FILE REFERENCE: 600-1-287N

; CURRENT FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US/10/027,828

; PRIOR FILING DATE: 2000-10-26

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 871

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-027-828-4

Query Match 99.9% Score 4573; DB 9; Length 871;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 869; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPCEVAELPGDESGTTCGGEAFPLSSLANLFEGEDGSLSPGADASRPPG 60

Db 1 MADSSGPRAGPCEVAELPGDESGTTCGGEAFPLSSLANLFEGEDGSLSPGADASRPPG 60

Qy 61 GDGRPNRMKFGQAFKRGVNPIDLLSTLYESSVWPGPKAPMDSLFDYGTGTYRHSSDN 120

Db 61 GDGRPNRMKFGQAFKRGVNPIDLLSTLYESSVWPGPKAPMDSLFDYGTGTYRHSSDN 120

Qy 121 KRWKTKTIEKQPSKAPAPQPPPIKAVENRPIFLDVSRGSTADLGLLPFLTLTKKRL 180

Db 121 KRWKTKTIEKQPSKAPAPQPPPIKAVENRPIFLDVSRGSTADLGLLPFLTLTKKRL 180

Qy 181 TDEEFREPSFGKTCCLPKALLNLSGRNDTIPVLDDIAERTGNMREFINSFPRDIYRGOT 240

Db 181 TDEEFREPSFGKTCCLPKALLNLSGRNDTIPVLDDIAERTGNMREFINSFPRDIYRGOT 240

Db 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
QY 241 ALHTAIERCKHYVELLYVAQADYHAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300  
Db 241 ALHVIERRCKHYVELLYVAQADYHAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300  
QY 301 VNYLTENPHKKADMRRODSRGNTVHLALVAIADNTRENTKFTVMYDGLLLKCARLPDS 360  
Db 301 VNYLTENPHKKADMRRODSRGNTVHLALVAIADNTRENTKFTVMYDGLLLKCARLPDS 360  
QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFOHIIIRREVTDEDTRHLSRKFKDWAYGPPVSSLYD 420  
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFOHIIIRREVTDEDTRHLSRKFKDWAYGPPVSSLYD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEIPINELLRDKWRKFGAVSYIINVSYLC 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEIPINELLRDKWRKFGAVSYIINVSYLC 480  
QY 481 AMVIFTLAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFFFTNIDLFMKKCPGV 540  
Db 481 AMVIFTLAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFFFTNIDLFMKKCPGV 540  
QY 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600  
Db 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600  
QY 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660  
Db 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660  
QY 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTYIILTFVLLNMLIALMGE 720  
Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTYIILTFVLLNMLIALMGE 720  
QY 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRV 780  
Db 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRRLRRDRWSSVPRVVELNKNSPDE 840  
Db 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRRLRRDRWSSVPRVVELNKNSPDE 840  
QY 841 VVYPLDSMGNPCDGHQGYPRKWRDADAP 870  
Db 841 VVYPLDSMGNPCDGHQGYPRKWRDADAP 870

## RESULT 2

us-10-000-823-7  
; Sequence 7, Application US/10000823  
; Publication No. US20030027164A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NO  
; TITLE OF INVENTION: HUMAN ION CHANNEL EXPRESSED IN SPINAL CORD AND BRAIN  
; FILE REFERENCE: D0109NP  
; CURRENT APPLICATION NUMBER: US/10/000,823  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/250,587  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 871  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
us-10-000-823-7

Query Match 99.9%; Score 4573; DB 9; Length 871;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 869; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADSEGPAGPCEVAELPGDESGTSGEAFPLSSLANLFEDEGSLSPSPADASRPAGP 60

Db 1 MADSEGPAGPCEVAELPGDESGTSGEAFPLSSLANLFEDEGSLSPSPADASRPAGP 60  
QY 61 GDGRPNLRMRKFOGAFRKGVPNPIDLLLESTLYESSVVPKPKAPMDSLFDYCTYRHSSDN 120  
Db 61 GDGRPNLRMRKFOGAFRKGVPNPIDLLLESTLYESSVVPKPKAPMDSLFDYCTYRHSSDN 120  
QY 121 KRWRKKIIEKQPOSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPLFLTHKKRL 180  
Db 121 KRWRKKIIEKQPOSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPLFLTHKKRL 180  
QY 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Db 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
QY 241 ALHTAIERCKHYVELLYVAQADYHAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300  
Db 241 ALHTAIERCKHYVELLYVAQADYHAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300  
QY 301 VNYLTENPHKKADMRRODSRGNTVHLALVAIADNTRENTKFTVMYDGLLLKCARLPDS 360  
Db 301 VNYLTENPHKKADMRRODSRGNTVHLALVAIADNTRENTKFTVMYDGLLLKCARLPDS 360  
QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFOHIIIRREVTDEDTRHLSRKFKDWAYGPPVSSLYD 420  
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFOHIIIRREVTDEDTRHLSRKFKDWAYGPPVSSLYD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEIPINELLRDKWRKFGAVSYIINVSYLC 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEIPINELLRDKWRKFGAVSYIINVSYLC 480  
QY 481 AMVIFTLAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFFFTNIDLFMKKCPGV 540  
Db 481 AMVIFTLAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFFFTNIDLFMKKCPGV 540  
QY 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600  
Db 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600  
QY 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660  
Db 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660  
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Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTYIILTFVLLNMLIALMGE 720  
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Db 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRRLRRDRWSSVPRVVELNKNSPDE 840  
Db 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRRLRRDRWSSVPRVVELNKNSPDE 840  
QY 841 VVYPLDSMGNPCDGHQGYPRKWRDADAP 870  
Db 841 VVYPLDSMGNPCDGHQGYPRKWRDADAP 870

## RESULT 3

us-10-027-828-2  
; Sequence 2, Application US/10027828  
; Publication No. US20030013650A1  
; GENERAL INFORMATION:  
; APPLICANT: Liedtke, Wolfgang  
; APPLICANT: Heller, Stefan  
; APPLICANT: Hudspeeth, Albert J.  
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC A  
; TITLE OF INVENTION: IT, AND USES THEREOF  
; FILE REFERENCE: 600-1-287N  
; CURRENT APPLICATION NUMBER: US/10/027,828

; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: US 60/243,568  
; PRIOR FILING DATE: 2000-10-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 871  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-10-027-828-2

Query Match 99.9%; Score 4571; DB 9; Length 871;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 868; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSEGPAGGVEAELPGDESGTGGGEAPPLSSLANLFEDEGSLSPSPADASRPPG 60  
Db 1 MADSEGPAGGVEAELPGDESGTGGGEAPPLSSLANLFEDEGSLSPSPADASRPPG 60  
Qy 61 GDGRPNLRMKFOGAFRGVNPIDLLESTLYESSVPGPKAPMDSLFYGYTHHSSDN 120  
Db 61 GDGRPNLRMKFOGAFRGVNPIDLLESTLYESSVPGPKAPMDSLFYGYTHHSSDN 120  
Qy 121 KRWKKTIEKQPOSPKAPAPQPPILKVFNRPIFLDIVSRGSTADLGLPFLTHKKRL 180  
Db 121 KRWKKTIEKQPOSPKAPAPQPPILKVFNRPIFLDIVSRGSTADLGLPFLTHKKRL 180  
Qy 181 TDEEFREPSGTCTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Db 181 TDEEFREPSGTCTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Qy 241 ALHAIERRCKHYVELLVAGADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNPHI 300  
Db 241 ALHAIERRCKHYVELLVAGADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNPHI 300  
Qy 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360  
Db 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360  
Qy 361 NLEAVLNDGLSPLMMAAKTKIGIFQHIIRREYTDTRHLSRKFQDWAYGVPVSSLYD 420  
Db 361 NLEAVLNDGLSPLMMAAKTKIGIFQHIIRREYTDTRHLSRKFQDWAYGVPVSSLYD 420  
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKKFGAVSFYINVSYLEC 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKKFGAVSFYINVSYLEC 480  
Qy 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDKMCKPGV 540  
Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDKMCKPGV 540  
Qy 541 NSLFDGSGFOLLFYIYSVLVSAALYLAGTEAVLVAVFALVGLWGNALYFTGLKLTG 600  
Db 541 NSLFDGSGFOLLFYIYSVLVSAALYLAGTEAVLVAVFALVGLWGNALYFTGLKLTG 600  
Qy 601 TYSIMIOKILFKDLFRLVYLLFMIGYASALVSLNPNCKMKNYCNEDQNTCTVPTPSC 660  
Db 601 TYSIMIOKILFKDLFRLVYLLFMIGYASALVSLNPNCKMKNYCNEDQNTCTVPTPSC 660  
Qy 661 RDSEFTFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
Db 661 RDSEFTFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
Qy 721 TVGQVSKESHIKLOWATITLIDERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
Db 721 TVGQVSKESHIKLOWATITLIDERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
Qy 781 DEVNWSHWNQNLGIIINEDPKNETYQYGFSTVGRLLRRORRWSVPRVVELNKNPNDE 840  
Db 781 DEVNWSHWNQNLGIIINEDPKNETYQYGFSTVGRLLRRORRWSVPRVVELNKNPNDE 840  
Qy 841 VVPLDSMGNPRCDGHOQGYPRKWRDTADP 870  
| | | | |

Db 841 VVPLDSMGNPRCDGHOQGYPRKWRDTADP 870

RESULT 4

US-10-090-215-7  
; Sequence 7, Application US/10090215  
; Publication No. US20030032097A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubin, Adrienne E  
; APPLICANT: Huvar, Arne  
; APPLICANT: Erlander, Mark G  
; APPLICANT: Glass, Charles A  
; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor  
; FILE REFERENCE: Human VR3  
; CURRENT APPLICATION NUMBER: US/10/090.215  
; CURRENT FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 871  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-10-090-215-7

Query Match 99.9%; Score 4571; DB 9; Length 871;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 869; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADSEGPAGGVEAELPGDESGTGGGEAPPLSSLANLFEDEGSLSPSPADASRPPG 60  
Db 1 MADSEGPAGGVEAELPGDESGTGGGEAPPLSSLANLFEDEGSLSPSPADASRPPG 60  
Qy 61 GDGRPNLRMKFOGAFRGVNPIDLLESTLYESSVPGPKAPMDSLFYGYTHHSSDN 120  
Db 61 GDGRPNLRMKFOGAFRGVNPIDLLESTLYESSVPGPKAPMDSLFYGYTHHSSDN 120  
Qy 121 KRWKKTIEKQPOSPKAPAPQPPILKVFNRPIFLDIVSRGSTADLGLPFLTHKKRL 180  
Db 121 KRWKKTIEKQPOSPKAPAPQPPILKVFNRPIFLDIVSRGSTADLGLPFLTHKKRL 180  
Qy 181 TDEEFREPSGTCTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Db 181 TDEEFREPSGTCTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Qy 241 ALHAIERRCKHYVELLVAGADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNPHI 300  
Db 241 ALHAIERRCKHYVELLVAGADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNPHI 300  
Qy 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360  
Db 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360  
Qy 361 NLEAVLNDGLSPLMMAAKTKIGIFQHIIRREYTDTRHLSRKFQDWAYGVPVSSLYD 420  
Db 361 NLEAVLNDGLSPLMMAAKTKIGIFQHIIRREYTDTRHLSRKFQDWAYGVPVSSLYD 420  
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKKFGAVSFYINVSYLEC 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKKFGAVSFYINVSYLEC 480  
Qy 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDKMCKPGV 540  
Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDKMCKPGV 540  
Qy 541 NSLFDGSGFOLLFYIYSVLVSAALYLAGTEAVLVAVFALVGLWGNALYFTGLKLTG 600  
Db 541 NSLFDGSGFOLLFYIYSVLVSAALYLAGTEAVLVAVFALVGLWGNALYFTGLKLTG 600  
Qy 601 TYSIMIOKILFKDLFRLVYLLFMIGYASALVSLNPNCKMKNYCNEDQNTCTVPTPSC 660  
Db 601 TYSIMIOKILFKDLFRLVYLLFMIGYASALVSLNPNCKMKNYCNEDQNTCTVPTPSC 660

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QY 661 RDSSTFSLDLFLKLTIGMGDLEMLSTKYPVVFIIILVYIILTFVLLNMLALMGE 720
DB 661 RDSSTFSLDLFLKLTIGMGDLEMLSTKYPVVFIIILVYIILTFVLLNMLALMGE 720
QY 721 TVGQVSKESKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCPRV 780
DB 721 TVGQVSKESKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCPRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGLRRDRWSSVVPVVELNKNNSPDE 840
DB 781 DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGLRRDRWSSVVPVVELNKNNSPDE 840
QY 841 VVPLDSMGNPRCDGHQOGYPRKWRRTDDAP 870
DB 841 VVPLDSMGNPRCDGHQOGYPRKWRRTDDAP 870

RESULT 5
US-10-227-255A-3
; Sequence 3, Application US/10227255A
; Publication No. US20030073117A1
; GENERAL INFORMATION:
; APPLICANT: Ishibashi, Ken'Ichi
; APPLICANT: Suzuki, Makoto
; TITLE OF INVENTION: No. US20030073117A1: Protein and Gene Encoding the Protein
; FILE REFERENCE: 10969/2032
; CURRENT APPLICATION NUMBER: US/10/227,255A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/JP01/01354
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP 048727/2000
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-227-255A-3

Query Match 99.3%; Score 4546; DB 9; Length 871;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 864; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MADSSEPRAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPAGP 60
DB 1 MADSSEPRAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPAGP 60
QY 61 GDRPNLRMKFQGAFRKGVNPNIDLESTLYESSVPGPKAPMDSLFDYGYTHHSSDN 120
DB 61 GDRPNLRMKFQGAFRKGVNPNIDLESTLYESSVPGPKAPMDSLFDYGYTHHSSDN 120
QY 121 KWRKKIIEKQPSKPAPQPPILKVFNRPIILFVSRGSTADLGLLPLFLTHKKRL 180
DB 121 KWRKKIIEKQPSKPAPQPPILKVFNRPIILFVSRGSTADLGLLPLFLTHKKRL 180
QY 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFROIYYRGQT 240
DB 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFROIYYRGQT 240
QY 241 ALHAIERRCKHYVELLVAOGADVHAQARGFFQPKDEGGYFYFGEGLPLSLAACTNPHI 300
DB 241 ALHAIERRCKHYVELLVAOGADVHAQARGFFQPKDEGGYFYFGEGLPLSLAACTNPHI 300
QY 301 VNYLTENPHKKADMRRODSRGNTVYHALVAIAONTRENTKFTVMYDLLLLKCARLPDS 360
DB 301 VNYLTENPHKKADMRRODSRGNTVYHALVAIAONTRENTKFTVMYDLLLLKCARLPDS 360
QY 361 NLEAVLNNDGLSPLMMAAKTKGIGFOHIIIRREVTDTRHLSKRFKDWAYGPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMMAAKTKGIGFOHIIIRREVTDTRHLSKRFKDWAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSEYINVSYLC 480
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DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSEYINVSYLC 480
QY 481 AMVIFTLAYQPLEGTPPYRTVDYLRLAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
DB 481 AMVIFTLAYQPLEGTPPYRTVDYLRLAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
QY 541 NSLFDGSQLLYFIYSVLVIVSAALYLAGEIAYLAVMVFAVLGLGMMNALYFTRGLKLTG 600
DB 541 NSLFDGSQLLYFIYSVLVIVSAALYLAGEIAYLAVMVFAVLGLGMMNALYFTRGLKLTG 600
QY 601 TYSIMIQILFKDLFRFLLYVLLFMIGYASALVSLNPCANKKVCNEDQTNCTVPTPSC 660
DB 601 TYSIMIQILFKDLFRFLLYVLLFMIGYASALVSLNPCANKKVCNEDQTNCTVPTPSC 660
QY 661 RDSSTFSLDLFLKLTIGMGDLEMLSTKYPVVFIIILVYIILTFVLLNMLALMGE 720
DB 661 RDSSTFSLDLFLKLTIGMGDLEMLSTKYPVVFIIILVYIILTFVLLNMLALMGE 720
QY 721 TVGQVSKESKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCPRV 780
DB 721 TVGQVSKESKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCPRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGLRRDRWSSVVPVVELNKNNSPDE 840
DB 781 DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGLRRDRWSSVVPVVELNKNNSPDE 840
QY 841 VVPLDSMGNPRCDGHQOGYPRKWRRTDDAP 870
DB 841 VVPLDSMGNPRCDGHQOGYPRKWRRTDDAP 870

RESULT 6
US-10-027-828-11
; Sequence 11, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeeth, Albert J.
; APPLICANT: Friedmann, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC A
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-027-828-11

Query Match 95.7%; Score 4378; DB 9; Length 871;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 825; Conservative 22; Mismatches 23; Indels 0; Gaps 0;

QY 1 MADSSEPRAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPAGP 60
DB 1 MADSSEPRAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPAGP 60
QY 61 GDRPNLRMKFQGAFRKGVNPNIDLESTLYESSVPGPKAPMDSLFDYGYTHHSSDN 120
DB 61 GDRPNLRMKFQGAFRKGVNPNIDLESTLYESSVPGPKAPMDSLFDYGYTHHSSDN 120
QY 121 KWRKKIIEKQPSKPAPQPPILKVFNRPIILFVSRGSTADLGLLPLFLTHKKRL 180
DB 121 KWRKKIIEKQPSKPAPQPPILKVFNRPIILFVSRGSTADLGLLPLFLTHKKRL 180
QY 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFROIYYRGQT 240
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181 TDEEFREPSTGKTCCLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRQT 240
QY
241 ALHTAIERCKHYVELLYVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
Db
241 ALHTAIERCKHYVELLYVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
QY
301 VNYLTENPHKKADRRQDSRGNTVLHALVAIADNTRENTKVTWKMYDILLKLCARLPDPS 360
Db
301 VNYLTENPHKKADRRQDSRGNTVLHALVAIADNTRENTKVTWKMYDILLKLCARLPDPS 360
QY
361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDWAYGVPVSSLYD 420
Db
361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDWAYGVPVSSLYD 420
QY
421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRKWKFKGAVSYINVSYLE 480
Db
421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRKWKFKGAVSYINVSYLE 480
QY
481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
Db
481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
QY
541 NSLFDGSGFQLLYFYISVLYVSAALYLAGIAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Db
541 NSLFDGSGFQLLYFYISVLYVSAALYLAGIAYLAVMVFALVGLWMNALYFTRGLKLTG 600
QY
601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660
Db
601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660
QY
661 RDSETFSAFLDLFLKLTIGMDLMSLSTKYPVVFVILLVYIILTFVLLNMLIALMGE 720
Db
661 RDSETFSAFLDLFLKLTIGMDLMSLSTKYPVVFVILLVYIILTFVLLNMLIALMGE 720
QY
721 TVGOVSKESKHIWKLQWATTILDIERSFPVFLKRAFRSGEMVTYKSSDGTDDRWCFRV 780
Db
721 TVGOVSKESKHIWKLQWATTILDIERSFPVFLKRAFRSGEMVTYKSSDGTDDRWCFRV 780
QY
781 DEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTVGLRRDRRWSSVVPVVELNKNPNDE 840
Db
781 DEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTVGLRRDRRWSSVVPVVELNKNPNDE 840
QY
841 VVPLDLSMGNPCDGHQOGYAPKWRDADAP 870
Db
841 VVPLDNLGNPCDGHQOGYAPKWRADAP 870
```

## RESULT 7

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US-10-227-255A-1
; Sequence 1, Application US/10227255A
; Publication No. US20030073117A1
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Makoto
; APPLICANT: Ishibashi, Ken'ichi
; TITLE OF INVENTION: No. US20030073117A1el Protein and Gene Encoding the Protein
; FILE REFERENCE: 10969/2032
; CURRENT APPLICATION NUMBER: US/10/227,255A
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/JP01/01354
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP 048727/2000
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-227-255A-1
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Query Match 95.6%; Score 4374; DB 9; Length 871;  
Best Local Similarity 94.8%; Pred. No. 0;

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Matches 825; Conservative 22; Mismatches 23; Indels 0; Gaps 0;
QY 1 MADSEGPACGGEVAELPGDESGTSGGEAPLSSLANLFECEGSLSPSADASRRPAGP 60
Db 1 MADPGDGPRAAPGEVAEPDDESGTSGGEAPLSSLANLFECEGSLSPSADASRRPAGP 60
QY 61 GDGRPNLRMKFQGAFAKGVNPNIDLESTLYESSVVGPKKAPMDSLDYGYRHHSSDN 120
Db 61 GDGRPNLRMKFQGAFAKGVNPNIDLESTLYESSVVGPKKAPMDSLDYGYRHHSSDN 120
QY 121 KRWRKKIIEKQFQSPKAPAPOPPPILKVFNPILFDIVSRGSTDADLGLLFLTHKKRL 180
Db 121 KRWRKVVYVEKQFQSPKTPAPOPPPILKVFNPILFDIVSRGSTDADLGLLFLTHKKRL 180
QY 181 TDEEFREPSTGKTCCLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRQT 240
Db 181 TDEEFREPSTGKTCCLPKALLNLSGRNDTLOVLLDIAERTGNMREFINSFPRDIYRQT 240
QY 241 ALHTAIERCKHYVELLYVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
Db 241 SLHTAIERCKHYVELLYVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADRRQDSRGNTVLHALVAIADNTRENTKVTWKMYDILLKLCARLPDPS 360
Db 301 VNYLTENPHKKADRRQDSRGNTVLHALVAIADNTRENTKVTWKMYDILLKLCARLPDPS 360
QY 361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDWAYGVPVSSLYD 420
Db 361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDWAYGVPVSSLYD 420
QY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRKWKFKGAVSYINVSYLE 480
Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRKWKFKGAVSYINVSYLE 480
QY 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
QY 541 NSLFDGSGFQLLYFYISVLYVSAALYLAGIAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Db 541 NSLFDGSGFQLLYFYISVLYVSAALYLAGIAYLAVMVFALVGLWMNALYFTRGLKLTG 600
QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660
Db 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660
QY 661 RDSETFSAFLDLFLKLTIGMDLMSLSTKYPVVFVILLVYIILTFVLLNMLIALMGE 720
Db 661 RDSETFSAFLDLFLKLTIGMDLMSLSTKYPVVFVILLVYIILTFVLLNMLIALMGE 720
QY 721 TVGOVSKESKHIWKLQWATTILDIERSFPVFLKRAFRSGEMVTYKSSDGTDDRWCFRV 780
Db 721 TVGOVSKESKHIWKLQWATTILDIERSFPVFLKRAFRSGEMVTYKSSDGTDDRWCFRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTVGLRRDRRWSSVVPVVELNKNPNDE 840
Db 781 DEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTVGLRRDRRWSSVVPVVELNKNPNDE 840
QY 841 VVPLDLSMGNPCDGHQOGYAPKWRDADAP 870
Db 841 VVPLDNLGNPCDGHQOGYAPKWRDADAP 870
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## RESULT 8

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US-10-027-828-10
; Sequence 10, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC
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; TITLE OF INVENTION: IT, AND USES THEREOF  
; FILE REFERENCE: 600-1-287N  
; CURRENT APPLICATION NUMBER: US/10/027,828  
; PRIOR FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: US 60/243,568  
; PRIOR FILING DATE: 2000-10-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 10  
; LENGTH: 871  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; US-10-027-828-10

Query Match 95.5%; Score 4372; DB 9; Length 871;  
Best Local Similarity 94.7%; Pred. No. 0;  
Matches 824; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGCEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPDASRPAGP 60  
Db 1 MADPGDGPRAAPGDAEPGDESGTSGGEAFPLSSLANLFEGEGSSLSPPVDASRPAGP 60

QY 61 GGRPNLRMKFOGAFKGVNPIDLLLESTLYESSVVPKPKAPMDSLDPDYGYRRHSSDN 120  
Db 61 GGRPNLRMKFOGAFKGVNPIDLLLESTLYESSVVPKPKAPMDSLDPDYGYRRHPSDN 120

QY 121 KWRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLLTHKKRL 180  
Db 121 KWRKKVVEKQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLLTHKKRL 180

QY 181 TDEEREPSTGKTCLPKALLNLSNRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGOT 240  
Db 181 TDEEREPSTGKTCLPKALLNLSNRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGOT 240

QY 241 ALHIAIERCKHYVELLVAGADVHAQAGRFFQPKDEGGYFYFGEPLSLAACNPHI 300  
Db 241 ALHIAIERCKHYVELLVAGADVHAQAGRFFQPKDEGGYFYFGEPLSLAACNPHI 300

QY 301 VNYLTENPHKKADMRRQDSRGNTVHLALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360  
Db 301 VNYLTENPHKKADMRRQDSRGNTVHLALVAIADNTRENTKFTVMYDLLLLKCSRLFPDS 360

QY 361 NLEAVLNNDGLSPLMMAAKTGIGIFQHIIRREVTDERTHLRSRKFOWAYGPVYSSLYD 420  
Db 361 NLEAVLNNDGLSPLMMAAKTGIGIFQHIIRREVTDERTHLRSRKFOWAYGPVYSSLYD 420

QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLROKWRKFGAVSFYINVSYL 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLROKWRKFGAVSFYINVSYL 480

QY 481 AMVIFTLTAYQPLEGTPPYRTVDYLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540  
Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540

QY 541 NSLFDGSGFOLLFIYISVLVVAALYLAGIEAYLAVMVFAVLVGMNALYFTRGLKLTG 600  
Db 541 NSLFDGSGFOLLFIYISVLVVAALYLAGIEAYLAVMVFAVLVGMNALYFTRGLKLTG 600

QY 601 TYSIMQIKFLKDLFRFLVLLFMIGYASALVSLNPNCKANMKVNEQDNTCTVPTPSC 660  
Db 601 TYSIMQIKFLKDLFRFLVLLFMIGYASALVTLNPNCKANMKVNEQDNTCTVPSYAC 660

QY 661 ROSETFTSLDLFLKLTGMGDMLESLSTKYPVWFIIILVTVIILTFVLLNMLALMGE 720  
Db 661 ROSETFSAFLDLFLKLTGMGDMLESLSSAKYPVWFIIILVTVIILTFVLLNMLALMGE 720

QY 721 TVGQVSKESKHILKQWATTIILDIERSFPVFLKAFRSGEMVTGKSSDGTDRWCFCRV 780  
Db 721 TVGQVSKESKHILKQWATTIILDIERSFPVFLKAFRSGEMVTGKSSDGTDRWCFCRV 780

QY 781 DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGRRLRRDRWSSVVPVWELNKNSPDE 840  
Db 781 DEVNWSHWNQNLGIINEDPGKSEIYYGFSHTVGRRLRRDRWSSVVPVWELNKNNGTDE 840

QY 841 VVYPLDSMGNPRCDGHQGYPRKWRDADAP 870  
Db 841 VVYPLDNLGNPNCDGHQGYAPKWRADAP 870

RESULT 9  
US-10-027-828-8  
; Sequence 8, Application US/10027828  
; Publication No. US20030013650A1  
; GENERAL INFORMATION:  
; APPLICANT: Liedtke, Wolfgang  
; APPLICANT: Heller, Stefan  
; APPLICANT: Hudspeth, Albert J.  
; APPLICANT: Friedman, Jeffrey M.  
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC  
; FILE REFERENCE: 600-1-287N  
; CURRENT APPLICATION NUMBER: US/10/027,828  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: US 60/243,568  
; PRIOR FILING DATE: 2000-10-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 8  
; LENGTH: 871  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; US-10-027-828-8

Query Match 95.5%; Score 4371; DB 9; Length 871;  
Best Local Similarity 94.7%; Pred. No. 0;  
Matches 824; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGCEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPDASRPAGP 60  
Db 1 MADPGDGPRAAPGDAEPGDESGTSGGEAFPLSSLANLFEGEGSSLSPPVDASRPAGP 60

QY 61 GGRPNLRMKFOGAFKGVNPIDLLLESTLYESSVVPKPKAPMDSLDPDYGYRRHSSDN 120  
Db 61 GGRPNLRMKFOGAFKGVNPIDLLLESTLYESSVVPKPKAPMDSLDPDYGYRRHPSDN 120

QY 121 KWRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLLTHKKRL 180  
Db 121 KWRKKVVEKQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLLTHKKRL 180

QY 181 TDEEREPSTGKTCLPKALLNLSNRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGOT 240  
Db 181 TDEEREPSTGKTCLPKALLNLSNRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGOT 240

QY 241 ALHIAIERCKHYVELLVAGADVHAQAGRFFQPKDEGGYFYFGEPLSLAACNPHI 300  
Db 241 ALHIAIERCKHYVELLVAGADVHAQAGRFFQPKDEGGYFYFGEPLSLAACNPHI 300

QY 301 VNYLTENPHKKADMRRQDSRGNTVHLALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360  
Db 301 VNYLTENPHKKADMRRQDSRGNTVHLALVAIADNTRENTKFTVMYDLLLLKCSRLFPDS 360

QY 361 NLEAVLNNDGLSPLMMAAKTGIGIFQHIIRREVTDERTHLRSRKFOWAYGPVYSSLYD 420  
Db 361 NLEAVLNNDGLSPLMMAAKTGIGIFQHIIRREVTDERTHLRSRKFOWAYGPVYSSLYD 420

QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLROKWRKFGAVSFYINVSYL 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLROKWRKFGAVSFYINVSYL 480

QY 481 AMVIFTLTAYQPLEGTPPYRTVDYLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540  
Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540

QY 541 NSLFDGSGFOLLFIYISVLVVAALYLAGIEAYLAVMVFAVLVGMNALYFTRGLKLTG 600  
Db 541 NSLFDGSGFOLLFIYISVLVVAALYLAGIEAYLAVMVFAVLVGMNALYFTRGLKLTG 600

Qy 601 TYSIMIKILFKDLFRELVLVYLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 660.  
Db 601 TYSIMIKILFKDLFRELVLVYLLFMIGYASALVLLNPNCTNMKVCNEDQSNCTVPSYPAC 660  
Qy 661 RDSFTFLLDLFKLIGMGDLMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
Db 661 RDSFTFAFLDLFKLIGMGDLMLSSAKYPVVFILLVYIILTFVLLNMLIALMGE 720  
Qy 721 TVGQVSKESHIKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCFRV 780  
Db 721 TVGQVSKESHIKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCFRV 780  
Qy 781 DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGRLLRRDRSSVPRVVELNKNSPDE 840  
Db 781 DEVNWSHWNQNLGIINEDPGKSEIYYGFSHTMGLRRDRSSVPRVVELNKNSGTDE 840  
Qy 841 VVPLDSMGNPRCDGHOOGYPRKWRDADAP 870  
Db 841 VVPLDLNLPNCNCDGHOOGYAPKWRADAP 870

RESULT 10

US-10-027-828-9

; Sequence 9, Application US/10027828

; Publication No. US20030013650A1

; GENERAL INFORMATION:

; APPLICANT: Liedtke, Wolfgang

; APPLICANT: Heller, Stefan

; APPLICANT: Hudspeth, Albert J.

; APPLICANT: Friedman, Jeffrey M.

; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS

; FILE REFERENCE: 600-1-287N

; CURRENT APPLICATION NUMBER: US/10/027,828

; PRIOR FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US 60/243,568

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 871

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-027-828-9

Query Match 95.58; Score 4371; DB 9; Length 871;  
Best Local Similarity 94.7%; Pred. No. 0;  
Matches 824; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRRPAG 60  
Db 1 MADPGDPRAAPGVAEPGDESGTSGEAPFLSSLANLFEDEGSSSLSPVDASRRPAG 60  
Qy 61 GDGRPNLRMKFOGAFRGVGNPIDLLESTLYESSVVPKPKAPMDSLFYGYTRHHSSDN 120  
Db 61 GDGRPNLRMKFOGAFRGVGNPIDLLESTLYESSVVPKPKAPMDSLFYGYTRHHSSDN 120  
Qy 121 KRWKPKKIEQPSQKAPAPQPPILKVFNPILFDIVSRGSTADLGLPLFLTHKKRL 180  
Db 121 KRWKPKKIEQPSQKAPAPQPPILKVFNPILFDIVSRGSTADLGLPLFLTHKKRL 180  
Qy 181 TDEFRPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Db 181 TDEFRPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Qy 241 ALHIAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300  
Db 241 ALHIAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300  
Qy 301 VNYLTENPHKADMRRDROSGNTVLHALVAIADNTRENTKFTKMYDLLLLKCARLPDS 360  
Db 301 VNYLTENPHKADMRRDROSGNTVLHALVAIADNTRENTKFTKMYDLLLLKCARLPDS 360

Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGI FOHIIRREVTDEDRHLRSKFKDWAYGVPVSSLYD 420  
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGI FOHIIRREVTDEDRHLRSKFKDWAYGVPVSSLYD 420  
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINNVSYLC 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINNVSYLC 480  
Qy 481 AMVIFTTATYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFKMKKCPGV 540  
Db 481 AMVIFTTATYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFKMKKCPGV 540  
Qy 541 NSLFDGSGFOLLFYIYSLVTVSAALYLAGIEAYLAVMVFALVGLWMNALYFTTGLKLTG 600  
Db 541 NSLFDGSGFOLLFYIYSLVTVSAALYLAGIEAYLAVMVFALVGLWMNALYFTTGLKLTG 600  
Qy 601 TYSIMIKILFKDLFRELVLVYLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 660  
Db 601 TYSIMIKILFKDLFRELVLVYLLFMIGYASALVLLNPNCTNMKVCNEDQSNCTVPSYPAC 660  
Qy 661 RDSFTFLLDLFKLIGMGDLMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
Db 661 RDSFTFAFLDLFKLIGMGDLMLSSAKYPVVFILLVYIILTFVLLNMLIALMGE 720  
Qy 721 TVGQVSKESHIKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCFRV 780  
Db 721 TVGQVSKESHIKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRWCFRV 780  
Qy 781 DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGRLLRRDRSSVPRVVELNKNSPDE 840  
Db 781 DEVNWSHWNQNLGIINEDPGKSEIYYGFSHTMGLRRDRSSVPRVVELNKNSGTDE 840  
Qy 841 VVPLDSMGNPRCDGHOOGYPRKWRDADAP 870  
Db 841 VVPLDLNLPNCNCDGHOOGYAPKWRADAP 870

RESULT 11

US-10-027-828-13

; Sequence 13, Application US/10027828

; Publication No. US20030013650A1

; GENERAL INFORMATION:

; APPLICANT: Liedtke, Wolfgang

; APPLICANT: Heller, Stefan

; APPLICANT: Hudspeth, Albert J.

; APPLICANT: Friedman, Jeffrey M.

; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC

; FILE REFERENCE: 600-1-287N

; CURRENT APPLICATION NUMBER: US/10/027,828

; PRIOR FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US 60/243,568

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 870

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-027-828-13

Query Match 94.7%; Score 4334.5; DB 9; Length 870;  
Best Local Similarity 94.4%; Pred. No. 0;  
Matches 821; Conservative 21; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MADSSGPRAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRRPAG 60  
Db 1 MADPGDPRAAPGVAEPGDESGTSGEAPFLSSLANLFEDEGSSSLSPVDASRRPAG 60  
Qy 61 GDGRPNLRMKFOGAFRGVGNPIDLLESTLYESSVVPKPKAPMDSLFYGYTRHHSSDN 120  
Db 61 GDGRPNLRMKFRSAFRGVGNPIDLLESTLYESSVVPKPKAPMDSLFYGYTRHHSSDN 120

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QY 121 KWRKKIIEKQSPKAPAPQPPILKVFNRPIPLDIVSRGSTADLDGLLFLTHKKRL 180
DB 121 KWRKKVVEKQSPKAPAPQPPILKVFNRPIPLDIVSRGSTADLDGLLFLTHKKRL 180
QY 181 TDEEFPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGOT 240
DB 181 TDEEFPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAOGADVHAQARGFQPKDEGGYFYEGELPLSLAACTNPHI 300
DB 241 SLHIAIERCKHYVELLVAOGADVHAQARGFQPKDEGGYFYEGELPLSLAACTNPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVYLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVYLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
QY 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFQDWAYGPVYSLYD 420
DB 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFQDWAYGPVYSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVSYLC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVSYLC 480
QY 481 AMWIFTLTAYYOQLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLPKMKCPGV 540
DB 481 AMWIFTLTAYYOQLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLPKMKCPGV 540
QY 541 NSLFDGSGFQLLYFIYSVLVSAALYLAGEAYLAVVAFVGLVGNMNAFYTRGLKLTG 600
DB 541 NSLFDGSGFQLLYFIYSVLVSAALYLAGEAYLAVVAFVGLVGNMNAFYTRGLKLTG 600
QY 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNLANPCANMKVCNEDQTNCTVPTPSC 660
DB 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNLANPCANMKVCNEDQTNCTVPTPAC 660
QY 661 RDETFSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720
DB 661 RDETFSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720
QY 721 TVGOVSKESKHIWKLOWATTILDIERSFPVFLRAFRSGEMVTVGKSSDGTDDRWCFRV 780
DB 721 TVGOVSKESKHIWKLOWATTILDIERSFPVFLRAFRSGEMVTVGKSSDGTDDRWCFRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRWSSVPRVVELNKNPNDE 840
DB 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRWSSVPRVVELNKNPNDE 840
QY 841 VVPLDSMGNPCDGHQOQYPRKWRDTDDAP 870
DB 840 VVPLDNLGNPCDGHQOQYAPKWRDTDDAP 869
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## RESULT 12

US-10-090-215-9

; Sequence 9, Application US/10090215

; Publication No. US20030032097A1

; GENERAL INFORMATION:

; APPLICANT: Dubin, Adrienne E

; APPLICANT: Huvar, Arne

; APPLICANT: Erlander, Mark G

; APPLICANT: Glass, Charles A

; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor

; FILE REFERENCE: Human VR3 receptors

; CURRENT APPLICATION NUMBER: US/10/090.215

; CURRENT FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 811

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-090-215-9

Query Match 92.2%; Score 4218; DB 9; Length 811;

Best Local Similarity 93.0%; Pred. No. 0;

Matches 809; Conservative 0; Mismatches 1; Indels 60; Gaps 1;

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QY 1 MADSEGPAGGVAELPGDESGTPGGEAPPLSLANLFEDEGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGVAELPGDESGTPGGEAPPLSLANLFEDEGSLSPSPADASRPAGP 60
QY 61 GDGPNLRMKFGGAFKGVNPNIDLLSTLYESSVVPKPKAPMDSLFDYGYTHHSSDN 120
DB 61 GDGPNLRMKFGGAFKGVNPNIDLLSTLYESSVVPKPKAPMDSLFDYGYTHHSSDN 120
QY 121 KWRKKIIEKQSPKAPAPQPPILKVFNRPIPLDIVSRGSTADLDGLLFLTHKKRL 180
DB 121 KWRKKIIEKQSPKAPAPQPPILKVFNRPIPLDIVSRGSTADLDGLLFLTHKKRL 180
QY 181 TDEEFPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGOT 240
DB 181 TDEEFPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAOGADVHAQARGFQPKDEGGYFYEGELPLSLAACTNPHI 300
DB 241 ALHIAIERCKHYVELLVAOGADVHAQARGFQPKDEGGYFYEGELPLSLAACTNPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVYLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVYLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
QY 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFQDWAYGPVYSLYD 420
DB 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFQDWAYGPVYSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVSYLC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVSYLC 480
QY 481 AMWIFTLTAYYOQLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLPKMKCPGV 540
DB 481 AMWIFTLTAYYOQLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLPKMKCPGV 540
QY 541 NSLFDGSGFQLLYFIYSVLVSAALYLAGEAYLAVVAFVGLVGNMNAFYTRGLKLTG 600
DB 541 NSLFDGSGFQLLYFIYSVLVSAALYLAGEAYLAVVAFVGLVGNMNAFYTRGLKLTG 600
QY 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNLANPCANMKVCNEDQTNCTVPTPSC 660
DB 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNLANPCANMKVCNEDQTNCTVPTPSC 660
QY 661 RDETFSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720
DB 661 RDETFSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720
QY 721 TVGOVSKESKHIWKLOWATTILDIERSFPVFLRAFRSGEMVTVGKSSDGTDDRWCFRV 780
DB 721 TVGOVSKESKHIWKLOWATTILDIERSFPVFLRAFRSGEMVTVGKSSDGTDDRWCFRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRWSSVPRVVELNKNPNDE 840
DB 721 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRWSSVPRVVELNKNPNDE 840
QY 841 VVPLDSMGNPCDGHQOQYPRKWRDTDDAP 870
DB 781 VVPLDSMGNPCDGHQOQYPRKWRDTDDAP 810
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## RESULT 13

US-09-764-367A-8

; Sequence 8, Application US/09764367A

; Patent No. US20020072101A1

; GENERAL INFORMATION:

```

; APPLICANT: Gaughan , Glen
; APPLICANT: Ramanathan, Chandra
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING CAT
; TITLE OF INVENTION: CHANNELS
; FILE REFERENCE: 5624.252.999
; CURRENT APPLICATION NUMBER: US/09/764,367A
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-367A-8

Query Match          91.7%; Score 4199; DB 10; Length 803;
Best Local Similarity 99.5%; Pred. No. 5.1e-318;
Matches 798; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 69 MKQGAARKGVPNPIDLLESTLYESSVPGPKAPMDSLFYGYRHHSSDNKRKKII 128
Db 1 MKQGAARKGVPNPIDLLESTLYESSVPGPKAPMDSLFYGYRHHSSDNKRKKII 60

Qy 129 EKOQSPKAPAPPPPIKVFNRPIILFDIVSRGSTDGLDGLLPFLTHKKRLTDEEPREP 188
Db 61 EKOQSPKAPAPPPPIKVFNRPIILFDIVSRGSTDGLDGLLPFLTHKKRLTDEEPREP 120

Qy 189 STGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOTALHIAIER 248
Db 121 STGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOTALHIAIER 180

Qy 249 RCHYVELLYVAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHVNYLTENP 308
Db 181 RCHYVELLYVAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHVNYLTENP 240

Qy 309 HKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLFPDSNLEAVLNN 368
Db 241 HKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLFPDSNLEAVLNN 300

Qy 369 DGLSPLMAAATCKIGIFQHIIRREVTDTRHLSRKFKOWAGPVVSYSLDLSLDTGC 428
Db 301 DGLSPLMAAATCKIGIFQHIIRREVTDTRHLSRKFKOWAGPVVSYSLDLSLDTGC 360

Qy 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAMVIFTLT 488
Db 361 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAMVIFTLT 420

Qy 489 AYQPLEGTPPYPTTVDYLRAGEVITLTGVLFFFTNIKDLFMKKCPGVNSLFDGGS 548
Db 421 AYQPLEGTPPYPTTVDYLRAGEVITLTGVLFFFTNIKDLFMKKCPGVNSLFDGGS 480

Qy 549 FOLLYFYISVLIVSAALYLAGIEAYLAVMVFAVLVGLMMNALYFTRGLKLTGTYSIMIQ 608
Db 481 FOLLYFYISVLIVSAALYLAGIEAYLAVMVFAVLVGLMMNALYFTRGLKLTGTYSIMIQ 540

Qy 609 ILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEQDNTCTVPTPSCRDSEFTST 668
Db 541 ILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEQDNTCTVPTPSCRDSEFTST 600

Qy 669 FLDLRLKLTGMGDMLESTKYPVVFIIILTVYIILTVFVLLNMLIALMGETVGVQSKE 728
Db 601 FLDLRLKLTGMGDMLESTKYPVVFIIILTVYIILTVFVLLNMLIALMGETVGVQSKE 660

Qy 729 SKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDRRCWCFRVDVNNKSHW 788
Db 661 SKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDRRCWCFRVDVNNKSHW 720

Qy 789 NONLGIINDEPGKNETYYGFSHTVGRRLRRDRSSVVPVRVELNKNNSNDEVVVPLDSM 848
Db 721 NONLGIINDEPGKNETYYGFSHTVGRRLRRDRSSVVPVRVELNKNNSNDEVVVPLDSM 780
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Qy 849 GNPRCDGHQOQGYPRKWRRTDDAP 870
Db 781 GNPRCDGHQOQGYPRKWRRTDDAP 802

RESULT 14
US-09-764-367A-2
; Sequence 2, Application US/09764367A
; Patent No. US20020072101A1
; GENERAL INFORMATION:
; APPLICANT: Gaughan , Glen
; APPLICANT: Ramanathan, Chandra
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODI
; TITLE OF INVENTION: CHANNELS
; FILE REFERENCE: 5624.252.999
; CURRENT APPLICATION NUMBER: US/09/764,367A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-21
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-367A-2

Query Match          90.4%; Score 4138; DB 10; Length 792;
Best Local Similarity 98.8%; Pred. No. 3e-313;
Matches 790; Conservative 0; Mismatches 2; Indels 8; Gaps 1;

Qy 69 MKQGAARKGVPNPIDLLESTLYESSVPGPKAPMDSLFYGYRHHSSDNKRKKII 128
Db 1 MKQGAARKGVPNPIDLLESTLYESSVPGPKAPMDSLFYGYRHHSSDNKRKKII 60

Qy 129 EKOQSPKAPAPPPPIKVFNRPIILFDIVSRGSTDGLDGLLPFLTHKKRLTDEEPREP 188
Db 61 EKOQSPKAPAPPPPIKVFNRPIILFDIVSRGSTDGLDGLLPFLTHKKRLTDEEPREP 120

Qy 189 STGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOTALHIAIER 248
Db 121 STGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOTALHIAIER 180

Qy 249 RCHYVELLYVAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHVNYLTENP 308
Db 181 RCHYVELLYVAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHVNYLTENP 240

Qy 309 HKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLFPDSNLEAVLNN 368
Db 241 HKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLFPDSNLEAVLNN 300

Qy 369 DGLSPLMAAATCKIGIFQHIIRREVTDTRHLSRKFKOWAGPVVSYSLDLSLDTGC 428
Db 301 DGLSPLMAAATCKIGIFQHIIRREVTDTRHLSRKFKOWAGPVVPSYDLSLDTGC 360

Qy 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAMVIFTLT 488
Db 361 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAMVIFTLT 420

Qy 489 AYQPLEGTPPYPTTVDYLRAGEVITLTGVLFFFTNIKDLFMKKCPGVNSLFDGGS 548
Db 421 AYQPLEGTPPYPTTVDYLRAGEVITLTGVLFFFTNIKDLFMKKCPGVNSLFDGGS 480

Qy 549 FOLLYFYISVLIVSAALYLAGIEAYLAVMVFAVLVGLMMNALYFTRGLKLTGTYSIMIQ 608
Db 481 FOLLYFYISVLIVSAALYLAGIEAYLAVMVFAVLVGLMMNALYFTRGLKLTGTYSIMIQ 540

Qy 609 ILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEQDNTCTVPTPSCRDSEFTST 668
Db 541 ILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEQDNTCTVPTPSCRDSEFTST 600

Qy 669 FLDLRLKLTGMGDMLESTKYPVVFIIILTVYIILTVFVLLNMLIALMGETVGVQSKE 728
Db 721 FLDLRLKLTGMGDMLESTKYPVVFIIILTVYIILTVFVLLNMLIALMGETVGVQSKE 728
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Db 601 FLDLFKLTIGMGDLEMLSTKYPVVFILLVTVIILTFVLLNMLIALMGETVQVSK 660
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Db 661 SKHIWKLOWATTIILDIERSPPVFLRKAFRSGEMTVGKSDGTDDRRCWCFVDEVNWSHW 720
Qy 789 NONLGIINEDEPGKNETQYGFSTVGRRLRRDRKSSVVPVVELNKNKNPDEVVPLDSM 848
Db 721 NONLGIINEDEPGKNETQYGFSTVGRRLRRDRKSSVVPVVELNKNKNPDEVVPLDSM 772
Qy 849 GNPDCDGHQOQYPRKWRD 868
Db 773 GNPDCDGHQOQYPRKWRD 792

RESULT 15
US-10-027-828-6
: Sequence 6, Application US/10027828
: Publication No. US20030013650A1
: GENERAL INFORMATION:
: APPLICANT: Liedtke, Wolfgang
: APPLICANT: Heller, Stefan
: APPLICANT: Hudspeth, Albert J.
: APPLICANT: Friedman, Jeffrey M.
: TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS
: TITLE OF INVENTION: IT AND USES THEREOF
: FILE REFERENCE: 600-1-287N
: CURRENT APPLICATION NUMBER: US/10/027,828
: CURRENT FILING DATE: 2001-10-25
: PRIOR APPLICATION NUMBER: US 60/243,568
: PRIOR FILING DATE: 2000-10-26
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patent in version 3.1
: SEQ ID NO 6
: LENGTH: 830
: TYPE: PRT
: ORGANISM: Rattus norvegicus
US-10-027-828-6
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Query Match 90.2%; Score 4127.5; DB 9; Length 830;

Best Local Similarity 90.0%; Pred. No. 2.le-312;

Matches 783; Conservative 23; Mismatches 23; Indels 41; Gaps 1;

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Db 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVYVPGPKAPMDSLFDTYRHHSSDN 120
Qy 121 KWRKKIIEKQOSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLPFLTHKKRL 180
Db 121 KWRKKVVEKQOSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLPFLTHKKRL 180
Qy 181 TDEEFREPSTGKTLCPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFDRDIYRGQT 240
Db 181 TDEEFREPSTGKTLCPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFDRDIYRGQT 240
Qy 241 ALHIAIERCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Db 241 ALHIAIERCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Qy 301 VNYLTENPHKKDMRRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLLKCARLPDS 360
Db 301 VNYLTENPHKKDMRRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLLKCARLPDS 360
Qy 361 NLEAVLNNDGLSPLMAAKTGKIGFQHIIRREVTDTPHLSRKEKDWAGVGYSSLYD 420
Db 361 NLEAVLNNDGLSPLMAAKTGKIGFQHIIRREVTDTPHLSRKEKDWAGVGYSSLYD 420
Qy 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVYSYLC 480
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Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVYSYLC 480
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Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFTTNIKDLEMKKCPGV 540
Qy 541 NSLFIDGSGFOLLFIYSVLVIVSAALYLAGIEAYLAYVWFALVGLWNNALYFTTGLKLTG 600
Db 541 NSLFIDGSGFOLLFIYSVLVIVSAALYLAGIEAYLAYVWFALVGLWNNALYFTTGLKLTG 600
Qy 601 TYSIMIOKILFKDLFRELLVLLFMIGYASALYSLNPNCANMKVCNEDQTNCTVPTVPS 660
Db 601 TYSIMIOKILFKDLFRELLVLLFMIGYASALYSLNPNCTNMKVCNEDQTNCTVPTVPS 660
Qy 661 RDSETFTFLDLFKLTIGMGDLEMLSTKYPVVFILLVTVIILTFVLLNMLIALMGE 720
Db 661 RDSETFTFLDLFKLTIGMGDLEMLSSAKYPVVFILLVTVIILTFVLLNMLIALMGE 720
Qy 721 TVGOVSKESKHINKLOWATTIILDIERSFPVFLKAFRSGEMTVGKSSDGTDDRRCWCFR 780
Db 721 TVGOVSKESKHINKLOWATTIILDIERSFPVFLKAFRSGEMTVGKSSDGTDDRRCWCFR 780
Qy 781 DEYNWSHWNONLGIINEDEPGKNETQYGFSTVGRRLRRDRKSSVVPVVELNKNKNPDE 840
Db 741 -QYNWSHWNONLGIINEDEPGKSELYQYGFSTVGRRLRRDRKSSVVPVVELNKNKSGTDE 799
Qy 841 VVYPLDSMGNPCDGHQOQYPRKWRD 870
Db 800 VVYPLDNLGNPCDGHQOQYPRKWRD 829
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Search completed: June 3, 2003, 19:57:03

Job time : 32 secs